

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 19, 2005, 08:37:45 ; Search time 174 Seconds  
(without alignments)  
273.697 Million cell updates/sec

Title: us-10-626-530-2

Perfect score: 93

Sequence: 1 MKISVAIPFLITLITLGT.....VCTNPSDKWQDYIKDKMKN 93

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1612378 seqs, 512079187 residues

Word size : 6

Total number of hits satisfying chosen parameters: 1316

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database : UniProt\_03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	93	100.0	93	1 SY14 HUMAN	Q16627 homo sapien
2	10	10.8	92	2 Q8HYQ3	Q8HYQ3 macaca mula
3	9	9.7	90	1 SY04 CHICK	Q90826 gallus gall
4	9	9.7	90	2 Q9PW46	Q9PW46 gallus gall
5	8	8.6	92	2 Q68A92	Q68A92 canis famil
6	8	8.6	115	2 Q8HHA0	Q8HHA0 cynocephalu
7	8	8.6	267	2 Q8UF11	Q8UF11 agrobacteri
8	8	8.6	288	2 Q7CYX2	Q7CYX2 agrobacteri
9	8	8.6	326	2 Q86207	Q86207 human rotav
10	8	8.6	818	2 Q7UR95	Q7UR95 rhodopirell
11	7	7.5	56	2 Q8HYN4	Q8HYN4 macaca mula
12	7	7.5	67	2 Q9VX52	Q9VX52 drosophila
13	7	7.5	68	2 Q7YX47	Q7YX47 caenorhabdi
14	7	7.5	82	2 Q9BZP4	Q9BZP4 homo sapien
15	7	7.5	92	1 SY03 HUMAN	P10147 h small ind
16	7	7.5	92	2 Q9MG95	Q9MG95 chrysodidym
17	7	7.5	93	1 SY03_BOVIN	Q8846 bos taurus
18	7	7.5	93	2 Q6DUR4	Q6DUR4 sus scrofa
19	7	7.5	115	2 Q66SX0	Q66SX0 diplometopo
20	7	7.5	116	2 Q85D00	Q85D00 platytrocte
21	7	7.5	118	2 Q8LX58	Q8LX58 cynocephalu
22	7	7.5	120	1 SY02_CAVPO	Q08782 cavia porce
23	7	7.5	162	1 RSD_SALTY	Q91916 salmonella
24	7	7.5	162	2 Q8Z327	Q8Z327 salmonella
25	7	7.5	214	2 Q7RU57	Q7RU57 neospora
26	7	7.5	221	2 Q8EPK2	Q8EPK2 oceanobacil
27	7	7.5	235	1 HXC6_HUMAN	P09630 homo sapien
28	7	7.5	235	1 HXC6_MOUSE	P10629 mus musculu
29	7	7.5	247	2 Q8TM45	Q8TM45 methanosarc
30	7	7.5	255	2 Q43332	Q43332 manduca sex
31	7	7.5	255	2 Q894P3	Q894P3 clostridium

#### ALIGNMENTS

32	7	7.5	265	2	Q86727	Q86727 sweet potat
33	7	7.5	289	2	Q8DKJ7	Q8DKJ7 synchococc
34	7	7.5	294	2	Q73ZS6	Q73ZS6 mycobacteri
35	7	7.5	314	2	Q9P3G9	Q9P3G9 neurospora
36	7	7.5	314	2	Q8IY42	Q8IY42 homo sapien
37	7	7.5	314	2	Q9NV03	Q9NV03 homo sapien
38	7	7.5	333	2	Q739T2	Q739T2 bacillus ce
39	7	7.5	335	2	Q81EK1	Q81EK1 bacillus ce
40	7	7.5	337	2	Q7RED0	Q7RED0 plasmodium
41	7	7.5	347	2	Q7RNI3	Q7RNI3 plasmodium
42	7	7.5	361	2	Q7RM26	Q7RM26 plasmodium
43	7	7.5	363	2	Q9RS42	Q9RS42 deinococcus
44	7	7.5	384	2	Q9LUT0	Q9LUT0 arabidopsis
45	7	7.5	381	2	Q755P8	Q755P8 ashbya goss
46	7	7.5	412	2	Q93EX5	Q93EX5 rhodococcus
47	7	7.5	416	2	Q9XE67	Q9XE67 sorghum bic
48	7	7.5	426	2	Q93JT5	Q93JT5 pseudomonas
49	7	7.5	427	2	Q9CNZ7	Q9CNZ7 pasteurella
50	7	7.5	427	2	Q9HU16	Q9HU16 pseudomonas
51	7	7.5	427	2	Q9I559	Q9I559 pseudomonas
52	7	7.5	428	2	Q6FTG1	Q6FTG1 candida gla
53	7	7.5	446	2	Q89RE3	Q89RE3 bradyrhizob
54	7	7.5	471	2	Q8UHS1	Q8UHS1 agrobacteri
55	7	7.5	474	2	Q8DYR2	Q8DYR2 streptococc
56	7	7.5	474	2	Q8E4B9	Q8E4B9 streptococc
57	7	7.5	485	2	Q68X88	Q68X88 rickettsia
58	7	7.5	486	2	Q9ZDP4	Q9ZDP4 rickettsia
59	7	7.5	487	2	Q7PBB3	Q7PBB3 rickettsia
60	7	7.5	487	2	Q92IN9	Q92IN9 rickettsia
61	7	7.5	494	1	AMYP_DROSU	Q18420 drosophila
62	7	7.5	499	2	Q9SS65	Q9SS65 arabidopsis
63	7	7.5	540	2	Q94C59	Q94C59 arabidopsis
64	7	7.5	540	2	Q9SA84	Q9SA84 arabidopsis
65	7	7.5	560	2	Q9TB51	Q9TB51 platyneireis
66	7	7.5	575	1	MBHL_WOLSU	P31883 wolinnella s
67	7	7.5	584	2	Q913I6	P31883 wolinnella s
68	7	7.5	616	2	Q8UAV6	Q8UAV6 agrobacteri
69	7	7.5	627	2	P74489	P74489 synchocyst
70	7	7.5	797	2	Q16824	Q16824 homo sapien
71	7	7.5	798	2	Q9H4U3	Q9H4U3 homo sapien
72	7	7.5	1567	2	Q6MIA1	Q6MIA1 bdellovibri
73	7	7.5	1726	2	Q6G4Z9	Q6G4Z9 bartonella
74	7	7.5	2850	1	HORN_HUMAN	Q86Y23 homo sapien
75	6	6.5	43	2	Q13384	Q13384 homo sapien
76	6	6.5	46	2	Q13385	Q13385 homo sapien
77	6	6.5	51	2	Q7RA10	Q7RA10 plasmodium
78	6	6.5	51	2	Q8FE64	Q8FE64 escherichia
79	6	6.5	58	2	Q9TSJ3	Q9TSJ3 cryptotogus
80	6	6.5	64	2	Q6H6S2	Q6H6S2 oryza sativ
81	6	6.5	68	2	Q8SXH7	Q8SXH7 drosophila
82	6	6.5	77	2	Q67TC2	Q67TC2 symbiobacte
83	6	6.5	77	2	Q93194	Q93194 african swi
84	6	6.5	77	2	Q9WLW7	Q9WLW7 african swi
85	6	6.5	78	2	Q93190	Q93190 african swi
86	6	6.5	78	2	Q65266	Q65266 african swi
87	6	6.5	78	2	Q9WLW6	Q9WLW6 african swi
88	6	6.5	80	2	Q14745	Q14745 homo sapien
89	6	6.5	80	2	Q6GXJ2	Q6GXJ2 gallus gall
90	6	6.5	80	2	Q9DC58	Q9DC58 gallus gall
91	6	6.5	82	1	9KO_HUMAN	P13994 homo sapien
92	6	6.5	84	2	Q6U287	Q6U287 homo sapien
93	6	6.5	84	2	Q7KPD3	Q7KPD3 caenorhabdi
94	6	6.5	84	2	Q804P1	Q804P1 pseudopleur
95	6	6.5	85	2	Q9XHG3	Q9XHG3 arabidopsis
96	6	6.5	87	1	PSK4_ARATH	Q98294 arabidopsis
97	6	6.5	87	2	Q7PCB9	Q7PCB9 arabidopsis
98	6	6.5	89	2	Q8C2W1	Q8C2W1 mus muscu
99	6	6.5	91	2	Q49892	Q49892 mycobacteri
100	6	6.5	92	1	SY04_MOUSE	P14097 mus musculu

RESULT 1  
 SY14 HUMAN  
 ID \_SY14 HUMAN STANDARD; PRT; 93 AA.  
 AC Q16627; Q13954;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Small inducible cytokine A14 precursor (CCL14) (Chemokine CC-1/CC-3)  
 DE (HCC-1/HCC-3) (HCC-1(1-74)) (NCC-2) [Contains: HCC-1(3-74); HCC-1(4-74); HCC-1(9-74)]  
 DE 74; HCC-1(9-74)]  
 GN Name=CCL14; Synonyms=NCC2, SCYA14;  
 OS Homo sapiens (Human)  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 [1]  
 RN SEQUENCE FROM N.A., AND SEQUENCE OF 20-93.  
 RC TISSUE=Bone marrow;  
 RX MEDLINE=96136773; PubMed=8551235;  
 RA Schulz-Knappe P., Maegert H.-J., Dewald B., Meyer M., Cetin Y.,  
 RA Kubbits M., Tomeczkowski J., Kirchhoff K., Raida M., Adermann K.,  
 RA Kist A., Reinecke N., Sillard R., Pardigol A., Uguccioni M.,  
 RA Baggolini M., Forssmann W.-G.;  
 RT "HCC-1, a novel chemokine from human plasma.";  
 RL J. Exp. Med. 183:295-299(1996).  
 [2]  
 RN SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=98263352; PubMed=9600961; DOI=10.1073/pnas.95.11.6308;  
 RA Pardigol A., Forssmann U., Zucht H.-D., Loetscher P.,  
 RA Schulz-Knappe P., Baggolini M., Forssmann W.-G., Maegert H.-J.;  
 RT "HCC-2, a human chemokine: gene structure, expression pattern, and  
 RT biological activity.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 95:6308-6313(1998).  
 [3]  
 RN SEQUENCE FROM N.A.  
 RX MEDLINE=99228475; PubMed=10213461; DOI=10.1089/107990993014153;  
 RA Nomiyama H., Fukuda S., Iio M., Tanase S., Miura R., Yoshie O.;  
 RT "Organization of the chemokine gene cluster on human chromosome  
 RT 17q11.2 containing the genes for CC chemokine MPIF-1, HCC-2, LEC, and  
 RT RANTES";  
 RL J. Interferon Cytokine Res. 19:227-234(1999).  
 [4]  
 RN SEQUENCE FROM N.A. (ISOFORM HCC-1).  
 RC TISSUE=Pancreas, and Spleen;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Heiton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.W., Green E.D., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Shevchenko Y., Bouffard G.G.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinska M.I., Skalek U., Smailus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 [5]  
 RN SEQUENCE OF 20-32, IDENTIFICATION OF HCC-1(3-74) AND HCC-1(4-74), MASS  
 RP SPECTROMETRY, AND CARBOHYDRATE-LINKAGE SITE SER-26.  
 RX PubMed=10978165; DOI=10.1021/bi992488q;  
 RA Richter R., Schulz-Knappe P., John H., Forssmann W.-G.;  
 RT "Posttranslationally processed forms of the human chemokine HCC-1.";

RL Biochemistry 39:10799-10805(2000).  
 RN [6]  
 RP SEQUENCE OF 20-48, IDENTIFICATION OF HCC-1(9-74), MASS SPECTROMETRY,  
 RP AND FUNCTION.  
 RX PubMed=11085751;  
 RA Dethoux M., Staendker L., Vakili J., Muench J., Forssmann U.,  
 RA Adermann K., Poehlmann S., Vassart G., Kirchhoff F., Parmentier M.,  
 RA Forssmann W.-G.;  
 RT "Natural proteolytic processing of hemofiltrate CC chemokine 1  
 RT generates a potent CC chemokine receptor (CCR)1 and CCR5 agonist with  
 RT anti-HIV properties";  
 RL J. Exp. Med. 192:1051-1058(2000).  
 CC -I- FUNCTION: Has weak activities on human monocytes and acts via  
 CC receptors that also recognize MIP-1 alpha. It induced  
 CC intracellular Ca(2+) changes and enzyme release, but no  
 CC chemotaxis, at concentrations of 100-1,000 nM, and was inactive on  
 CC T lymphocytes, neutrophils, and eosinophil leukocytes. Enhances  
 CC the proliferation of CD34 myeloid progenitor cells. The processed  
 CC form HCC-1(9-74) is a chemotactic factor that attracts monocytes  
 CC eosinophils, and T-cells and is a ligand for CCR1, CCR3 and CCR5.  
 CC -I- SUBCELLULAR LOCATION: Secreted.  
 CC -I- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Name=HCC-1;  
 CC IsoId=Q16627-1; Sequence=Displayed;  
 CC Name=HCC-3;  
 CC IsoId=Q16627-2; Sequence=VSP\_001060;  
 CC -I- TISSUE SPECIFICITY: Expressed constitutively in several normal  
 CC tissues: spleen, liver, skeletal and heart muscle, gut, and bone  
 CC marrow, present at high concentrations (1-80 nM) in plasma.  
 CC -I- PTM: The N-terminal processed forms HCC-1(3-74), HCC-1(4-74) and  
 CC HCC-1(9-74) are produced in small amounts by proteolytic cleavage  
 CC after secretion in blood.  
 CC -I- PTM: HCC-1(1-74), but not HCC-1(3-74) and HCC-1(4-74), is  
 CC partially O-glycosylated; the O-linked glycan consists of one Gal-  
 CC GalNAc disaccharide, further modified by two N-acetylneuraminic  
 CC acids.  
 CC -I- SIMILARITY: Belongs to the intercrine beta (chemokine CC) family.  
 -----  
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 -----  
 CC EMBL; Z49270; CAA89264.1; -;  
 DR EMBL; Z70292; CAA94307.1; -;  
 DR EMBL; Z70293; CAA94309.1; -;  
 DR EMBL; Z49269; CAA89263.1; -;  
 DR EMBL; AF088219; AAC63329.1; -;  
 DR EMBL; AF088219; AAF23982.1; -;  
 DR EMBL; BC045165; AAH45165.1; -;  
 DR HSSP; P13236; 1HUM.  
 DR Genew; HGNC:10612; CCL14.  
 DR MIM; 601392; -;  
 DR GO; GO:0005615; C:extracellular space; TAS.  
 DR GO; GO:0004871; F:signal transducer activity; TAS.  
 DR GO; GO:0006874; P:calcium ion homeostasis; TAS.  
 DR GO; GO:0008284; P:positive regulation of cell proliferation; TAS.  
 DR InterPro; IPR000827; CC chemokine sm1.  
 DR InterPro; IPR001811; Chemokine\_IL8.  
 DR Pfam; PF00048; IL8; 1  
 DR PROSITE; PS00472; SMALL\_CYTOKINES\_CC; 1.  
 DR Alternative splicing; Cytokine; Direct protein sequencing;  
 KW Glycoprotein; Signal.  
 FT SIGNAL 1 19  
 FT CHAIN 20 93 Small inducible cytokine A14.  
 FT CHAIN 22 93 HCC-1(3-74).  
 FT CHAIN 23 93 HCC-1(4-74).  
 FT CHAIN 28 93 HCC-1(9-74).  
 FT DISULFID 35 59 By similarity.

```
FT DISULFID 36 75 By similarity.
FT CARBOHYD 26 26 O -> OTGGKPKVVKIQLKLG (in isoform HCC-
FT VARSPLIC 27 27 3).
FT FT
FT SEQUENCE 93 AA; 10678 MW; DDB899DC9148836 CRC64;
Query Match 100.0%; Score 93; DB 1; Length 93;
Best Local Similarity 100.0%; Pred. No. 4.9e-94;
Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MKISVAIPFLLITIALGTETSSSRGPHVPSGCCFTYTKIPRIMDYETNSQCS 60
Db 1 MKISVAIPFLLITIALGTETSSSRGPHVPSGCCFTYTKIPRIMDYETNSQCS 60
Qy 61 KPGIVFITKRGHSVCTNPSPDKWQDYIKDMKEN 93
Db 61 KPGIVFITKRGHSVCTNPSPDKWQDYIKDMKEN 93
RESULT 2
Q8HYQ3 PRELIMINARY; PRT; 92 AA.
AC Q8HYQ3
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Chemokine CCL3/MIP-1ALPHA.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22123042; PubMed=12126650; DOI=10.1006/cyto.2002.0875;
RA Basu S., Schaefer T.M., Ghosh M., Fuller C.L., Reinhart T.A.;
RT "Molecular cloning and sequencing of 25 different rhesus macaque
RT chemokine cDNAs reveals evolutionary conservation among C, CC, CX,
RT AND CX3C families of chemokines.";
RL Cytokine 18:140-148(2002)
DR EMBL; AF449266; AAN76070.1; -.
DR HSP; P10147; I850.
DR GO; GO:000576; C:extracellular; IEA.
DR GO; GO:0008009; F:chemokine activity; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR000827; CC_chemkine_sml.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR SMART; SM00199; SCY; 1.
DR PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
SQ SEQUENCE 92 AA; 10120 MW; 021CAA371143D12A CRC64;
Query Match 10.8%; Score 10; DB 2; Length 92;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 54 ETNSQCSKPG 63
Db 52 ETNSQCSKPG 61
RESULT 3
SY04_CHICK STANDARD; PRT; 90 AA.
AC SY04_CHICK
DT 01-NOV-1997 (Rel. 35, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Small inducible cytokine A4 homolog precursor (Macrophage inflammatory
DE protein 1-beta homolog).
GN Name=CCL4; Synonyms=SCYA4;
OS Gallus gallus (Chicken).
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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Bone marrow;
RX MEDLINE=95369710; PubMed=7642115; DOI=10.1016/0378-1119(95)00210-W;
RA Petrenko O., Ichenko I., Enrietto P.J.;
RT "Isolation of a cDNA encoding a novel chicken chemokine homologous to
RT mammalian macrophage inflammatory protein-1 beta.";
RL Gene 160:305-306(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20049023; PubMed=10582310;
RA Hughes S., Bumstead N.;
RT "Mapping of the gene encoding a chicken homologue of the mammalian
RT chemokine SCYA4.";
RL Anim. Genet. 30:404-404(1999).
RN [3]
RP SEQUENCE OF 14-90 FROM N.A.
RA Petrenko O., Enrietto P.J.;
RA Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Monokine with inflammatory and chemokinetic properties
CC (By similarity).
CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the intercrine beta (chemokine CC) family.
CC
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CC
CC EMBL; L34553; AAA48747.1; -.
CC EMBL; AJ243034; CAB45103.1; -.
CC HSP; P13236; IHUM.
CC InterPro; IPR000827; CC_chemkine_sml.
CC InterPro; IPR001811; Chemokine_IL8.
CC Pfam; PF00048; IL8; 1.
CC PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
CC Chemotaxis; Cytokine; Signal.
KW CHAIN 1 21 By similarity.
FT CHAIN 22 90 Small inducible cytokine A4 homolog.
FT DISULFID 32 56 By similarity.
FT DISULFID 33 72 By similarity.
FT CONFLICT 87 87 M -> L (in Ref. 1).
SQ SEQUENCE 90 AA; 9987 MW; 50AF9679A267408F CRC64;
Query Match 9.7%; Score 9; DB 1; Length 90;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 51 DYETNSQC 59
Db 48 DYETNSQC 56
RESULT 4
Q9PWA6 PRELIMINARY; PRT; 90 AA.
AC Q9PWA6
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Chemokine.
GN Name=SCYA4;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Hughes S.M., Bumstead N.;
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF146730; AAD48772.1; -.
DR HSSP; P13236; 1HUM.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008009; P:chemokine activity; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR000827; CC_chemokine_sml.
DR DR InterPro; IPR001811; Chemokine_IL8.
DR PFam; PF00048; IL8; 1.
DR SMART; SM00199; SCV; 1.
DR PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
SQ SEQUENCE 90 AA; 9986 MW; 50AF9679A26751CB CRC64;

Query Match 9.7%; Score 9; DB 2; Length 90;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 DYETNSQC 59
Db |||||
48 DYETNSQC 56

RESULT 5
Q68A92
ID Q68A92 PRELIMINARY; PRT; 92 AA.
AC Q68A92;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE CC chemokine ligand 3.
GN Name=CCCL3;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RA Tsukui T., Sakaguchi M., Maeda S., Koyanagi M., Masuda K., Ohno K.,
RA Tsujimoto H., Iwabuchi S.;
RT "Expression analysis of gene in canine atopic dermatitis.";
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB164618; BAD42447.1; -.
DR InterPro; IPR001811; Chemokine_IL8.
DR PFam; PF00048; IL8; 1.
DR SMART; SM00199; SCV; 1.
SQ SEQUENCE 92 AA; 10029 MW; 9D44596B37FD6910 CRC64;

Query Match 8.6%; Score 8; DB 2; Length 92;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 57 SQCSKPGI 64
Db |||||
55 SQCSKPGI 62

RESULT 6
Q8HHA0
ID Q8HHA0 PRELIMINARY; PRT; 115 AA.
AC Q8HHA0;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE NADH subunit 3.
OS Cynocephalus variegatus (Flying lemur).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Dermoptera; Cynocephalidae; Cynocephalus.

OX NCBI_TaxID=9457;
RN [1]
RP SEQUENCE FROM N.A.
RA Schmitz J., Ohme M., Suryobroto B., Zischler H.;
RT "The colugo (Cynocephalus variegatus, Dermoptera): the primates'
RT gliding sister?";
RL Mol. Biol. Evol. 19:2308-2312(2002).
CC 1- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
CC 1- SIMILARITY: Belongs to the complex I subunit 3 family.
DR EMBL; AF460846; AAN84904.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
DR GO; GO:0008137; F:NADH dehydrogenase (ubiquinone) activity; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006120; P:mitochondrial electron transport, NADH to u. . .; IEA.
DR InterPro; IPR000440; Oxidored_q4.
DR PFam; PF00507; Oxidored_q4; 1.
DR KW Mitochondrion; NAD; Oxidoreductase; Ubiquinone.
SQ SEQUENCE 115 AA; 13041 MW; DE6CDE362DD15DA5 CRC64;

Query Match 8.6%; Score 8; DB 2; Length 115;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 FLLITIAL 18
Db |||||
15 FLLITIAL 22

RESULT 7
Q8UF11
ID Q8UF11 PRELIMINARY; PRT; 267 AA.
AC Q8UF11;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein Atul591.
GN OrderedLocNames=Atul591;
OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
OX NCBI_TaxID=176299;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=Dupont;
RC MEDLINE=21608550; PubMed=11743193; DOI=10.1126/science.1066804;
RA Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
RA Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
RA Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,
RA Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
RA Kutayavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,
RA Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,
RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
RA Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
RA Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
RA Nester E.W.;
RT "The genome of the natural genetic engineer Agrobacterium tumefaciens
RT C58.";
RL Science 294:2317-2323(2001).
DR EMBL; AB009116; AAL42593.1; -.
DR PIR; AC2772; AC2772.
DR PIR; B97552; B97552.
DR PFam; PF01925; DUF81; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 267 AA; 28091 MW; CCDF37F1F6C84F6C CRC64;

Query Match 8.6%; Score 8; DB 2; Length 267;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 FLLITIAL 18
Db |||||
109 FLLITIAL 116

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RESULT 8
Q7CYX2 PRELIMINARY; PRT; 288 AA.
AC Q7CYX2, 2004 (Tremblrel. 27, Created)
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
DE AGR C 2926p.
GN OrderedLocusNames=AGR C 2926;
OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
OX NCBI_TaxID=176299;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Cereon;
RX MEDLINE=21608551; PubMed=11743194; DOI=10.1126/science.1066803;
RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
RA Qurollo B., Goldman B.S., Cao Y., Akenazi M., Halling C., Mullin L.,
RA Houmieu K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,
RA Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
RA Planagan C., Crowell C., Gursen J., Lomo C., Sear C., Strub G.,
RA Cielo C., Slater S.;
RT "Genome sequence of the plant pathogen and biotechnology agent
RT Agrobacterium tumefaciens C58."
RL Science 294:2323-2328(2001).
DR EMBL: AE008081; AAK87371.1; -.
DR InterPro: IPR002781; DUF81.
DR Pfam: PF01925; DUF81; 1.
SQ SEQUENCE 288 AA; 30488 MW; 25BB853798BD147D7 CRC64;

Query Match 8.6%; Score 8; DB 2; Length 288;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 FLITIAL 18
Db 130 FLITIAL 137

RESULT 9
Q86207 PRELIMINARY; PRT; 326 AA.
AC Q86207, 1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-NOV-1996 (Tremblrel. 02, Last annotation update)
DE VP7.
OS Human rotavirus II type 1.
OC Viruses; dsRNA viruses; Reoviridae; Rotavirus; Human rotavirus A;
OC Human rotavirus 2.
OX NCBI_TaxID=36432;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K8;
RX MEDLINE=89342660; PubMed=2474677;
RA Taniguchi K., Nishikawa K., Urasawa T., Urasawa S., Midthun K.,
RA Kapikian A.Z., Gorziglia M.;
RT "Complete nucleotide sequence of the gene encoding VP4 of a human
RT rotavirus (strain K8) which has unique VP4 neutralization epitopes."
RL J. Virol. 63:4101-4106(1989).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K8;
RA Taniguchi K.;
RL Submitted (JUN-1993) to the EMBL/GenBank/DBJ databases.
DR EMBL: D16344; BAA03848.1; -.
DR GO: GO:0019028; C:viral capsid; IEA.
DR InterPro: IPR001963; VP7.
DR Pfam: PF00434; VP7; 1.
DR ProDom: PD000191; VP7; 1.

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SQ SEQUENCE 326 AA; 37371 MW; 998F7C5D8722C87 CRC64;

Query Match 8.6%; Score 8; DB 2; Length 326;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 FLITIAL 18
Db 37 FLITIAL 44

RESULT 10
Q7UR95 PRELIMINARY; PRT; 818 AA.
AC Q7UR95, 2003 (Tremblrel. 25, Created)
DT 01-OCT-2003 (Tremblrel. 25, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Polyrribonucleotide nucleosidyltransferase (EC 2.7.7.8).
GN Name=ppp; OrderedLocusNames=RB5804;
OS Rhodopirella baltica.
OC Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;
OC Planctomycetaceae; Pirellula.
OX NCBI_TaxID=117;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1;
RX MEDLINE=22735913; PubMed=12835416; DOI=10.1073/pnas.1431443100;
RA Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T.,
RA Ludwig W., Gade D., Beck A., Borzym K., Heitmann K., Rabus R.,
RA Schlesner H., Amann R., Reinhardt R.;
RT "Complete genome sequence of the marine planctomycete Pirellula sp.
RT strain 1."
RL Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303(2003).
DR EMBL: BX294143; CAD74445.1; -.
DR HSP: Q53597; IE3P.
DR GO: GO:0000175; F:3'-5'-exoribonuclease activity; IEA.
DR GO: GO:0004654; F:polyribonucleotide nucleosidyltransferase a. . .; IEA.
DR GO: GO:0003723; F:RNA binding; IEA.
DR GO: GO:0016740; F:transferase activity; IEA.
DR GO: GO:0006396; P:RNA processing; IEA.
DR InterPro: IPR001247; 3 ExorNase.
DR InterPro: IPR004087; KH.
DR InterPro: IPR004088; KH_type_1.
DR Pfam: PF00013; KH_1; 1.
DR Pfam: PF03726; PNase_1.
DR Pfam: PF01138; RNase_PH; 2.
DR Pfam: PF03725; RNase_PH_C; 2.
DR Pfam: PF00575; S1; 1.
DR SMART: SM00322; KH; 1.
DR SMART: SM00316; S1; 1.
DR PROSITE: PS50084; KH_TYPE_1; 1.
DR PROSITE: PS50126; S1; 1.
KW Complete proteome; Nucleosidyltransferase; Transferase.
SQ SEQUENCE 818 AA; 88221 MW; 1A57F962C413B17A CRC64;

Query Match 8.6%; Score 8; DB 2; Length 818;
Best Local Similarity 100.0%; Pred. No. 9.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 LITIALGT 20
Db 417 LITIALGT 424

RESULT 11
Q8HYN4 PRELIMINARY; PRT; 56 AA.
AC Q8HYN4, 2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 25, Last annotation update)

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DE Macrophage inflammatory protein 1 alpha (Fragment).  
OS *Macaca mulatta* (Rhesus macaque).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
OC Cercopithecoidea; Cercopithecoidea; Cercopithecoidea;  
OX NCBI\_TaxID=9544;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22074459; PubMed=12079558; DOI=10.1089/08922202760019329;  
RA Hofmann-Lehmann R., Williams A.L., Swenerton R.K., Li P.-L.,  
RA Rasmussen R.A., Chenine A.-L., McClure H.W., Ruprecht R.M.;  
RT "Quantitation of simian cytokine and beta-chemokine mRNAs, using real-  
RT time reverse transcriptase-polymerase chain reaction: variations in  
RT expression during chronic primate lentivirus infection.";  
RL AIDS Res Hum Retroviruses 18:627-639(2002).  
DR EMBL; AF457195; AAN76985.1; -;  
DR HSSP; P10147; IB50.  
DR GO; GO:0005576; C:extracellular; IEA.  
DR GO; GO:0008009; F:chemokine activity; IEA.  
DR GO; GO:0006955; P:immune response; IEA.  
DR InterPro; IPR000827; CC chemokine sm.  
DR InterPro; IPR001811; Chemokine\_I58.  
DR Pfam; PF00048; IL8; 1.  
DR SMART; SM00199; SCY; 1.  
DR PROSITE; PS00472; SMALL\_CYTOKINES\_CC; 1.  
FT NON\_TER 1 56  
FT TER 56  
SQ SEQUENCE 56 AA; 6442 MW; EB12A0E0D41D5F68 CRC64;  
Query Match 7.5%; Score 7; DB 2; Length 56;  
Best Local Similarity 100.0%; Pred. No. 15;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 57 SQCSKPG 63  
DB 26 SQCSKPG 32  
RESULT 12  
Q9VX52 PRELIMINARY; PRT; 67 AA.  
AC Q9VX52;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)  
DE G12994-PA.  
GN ORFNames=CG12994;  
OS *Drosophila melanogaster* (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7227;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;  
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
RA Ananides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,  
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
RA Brandon R.C., Rogers Y.H., Blazer R.G., Champe M., Pfeiffer B.D.,  
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,  
RA Abail J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,  
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,  
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
RA Dodson K., Dou P.L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrieria S., Fleischmann W.,  
RA Foeller C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,  
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,  
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,  
RA Shue B.C., Siden-Kianos I., Simpson M., Skupski M.P., Smith T.,  
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
RA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
RA Wang Z.Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,  
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,  
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
RT "The genome sequence of *Drosophila melanogaster*.";  
RL Science 287:2185-2195(2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22426065; PubMed=12537568;  
RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,  
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,  
RA George R.A., Hoskins R.A., Lavery T., Muzny D.M., Nelson C.R.,  
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,  
RA Swirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,  
RA Weinstein G., Scher S.E., Myers E.W., Gibbs R.A., Rubin G.M.;  
RT "Finishing a whole-genome shotgun: Release 3 of the *Drosophila*  
RT melanogaster euchromatic genome sequence.";  
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22426070; PubMed=12537573;  
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Swirskas R.,  
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,  
RA Ashburner M., Celniker S.E.;  
RT "The transposable elements of the *Drosophila melanogaster* euchromatin:  
RT a genomic perspective.";  
RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).  
RN [4]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22426069; PubMed=12537572;  
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,  
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,  
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,  
RA Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,  
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,  
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,  
RA Lewis S.E.;  
RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a  
RT systematic review.";  
RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).  
RN [5]  
RP SEQUENCE FROM N.A.  
RG FlyBase;  
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.  
RN [6]  
RP SEQUENCE FROM N.A.  
RG FlyBase;  
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.  
RL EMBL; AS003505; AAF48728.1; -;  
DR IntAct; Q9VX52; -;  
DR FlyBase; Fgn0040877; CGI2994;  
SQ SEQUENCE 67 AA; 7578 MW; 27EDCC7A294303BE CRC64;  
Query Match 7.5%; Score 7; DB 2; Length 67;  
Best Local Similarity 100.0%; Pred. No. 17;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 12 LITIAL 18  
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Db 42 LLINITIAL 48
RESULT 13
Q7YX47 PRELIMINARY; PRT; 68 AA.
AC Q7YX47;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein C38C10.6.
GN ORENAMES=C38C10.6;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
investigating biology.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Thomas K.;
RL Submitted (DSC-1992) to the EMBL/GenBank/DBJ databases.
DR EMBL: Z19153; CAEL17766.1; -.
DR WormBase; WBGene00008002; C38C10.6.
DR WormPep; C38C10.6; CE34740.
KW Hypothetical protein.
SQ SEQUENCE 68 AA; 7893 MW; 5DF6271284D43973 CRC64;

Query Match 7.5%; Score 7; DB 2; Length 68;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 LLINITIAL 18
Db 12 LLINITIAL 18
RESULT 14
Q9BZP4 PRELIMINARY; PRT; 82 AA.
AC Q9BZP4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Putative C18orf2 variant 1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Retina;
RX MEDLINE=21098486; PubMed=11173869;
RA Stohr H., Mah N., Schulz H.L., Gehrig A., Frohlich S., Weber B.H.;
RT "EST mining of the Unigene dataset to identify retina-specific
genes.";
RL Cytogenet. Cell Genet. 91:267-277(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Retina;
RA Stohr H., Schulz H.L., Mah N., Gehrig A., Froehlich S., Weber B.H.F.;
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF295726; AAK13319.1; -.
SQ SEQUENCE 82 AA; 9406 MW; 5162CA14CED467B5 CRC64;

Query Match 7.5%; Score 7; DB 2; Length 82;
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Best Local Similarity 100.0%; Pred. No. 20;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 LLINITIAL 18
Db 21 LLINITIAL 27
RESULT 15
SY03 HUMAN
ID SY03 HUMAN STANDARD; PRT; 92 AA.
AC P10147;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Small inducible cytokine A3 precursor (CC13) (Macrophage inflammatory
protein 1-alpha) (MIP-1-alpha) (Tonsillar lymphocyte LD78 alpha
protein) (G0/G1 switch regulatory protein 19-1) (GOS19-1 protein)
DE (SIS-beta) (PAT 464.1) [Contains: MIP-1-alpha(4-69) (LD78-alpha(4-
69))].
DE [69]].
GN Names=CC13; Synonyms=GOS19-1, MIP1A, SCYA3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86223879; PubMed=3086300;
RA Obaru K., Fukuda M., Maeda S., Shimada K.;
RT "A cDNA clone used to study mRNA inducible in human tonsillar
lymphocytes by a tumor promoter.";
RL J. Biochem. 99:885-894(1986).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=89140347; PubMed=2521882;
RA Zipfel P.F., Balke J., Irving S.G., Kelly K., Siebenlist U.;
RT "Mitogenic activation of human T cells induces two closely related
genes which share structural similarities with a new family of
secreted factors.";
RL J. Immunol. 142:1582-1590(1989).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=91103879; PubMed=22711120;
RA Blum S., Forsdyke R.E., Forsdyke D.R.;
RT "Three human homologs of a murine gene encoding an inhibitor of stem
cell proliferation.";
RL DNA Cell Biol. 9:589-602(1990).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=90287155; PubMed=1694014;
RA Nakao M., Nomiya H., Shimada K.;
RT "Structures of human genes coding for cytokine LD78 and their
expression.";
RL Mol. Cell. Biol. 10:3646-3658(1990).
RN [5]
RP SEQUENCE OF 23-92 FROM N.A.
RA Jang J.S., Kim B.E.;
RT Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE OF 24-92, AND MUTAGENESIS OF ASP-49.
RX MEDLINE=96127782; PubMed=8541527;
RA Hunter M.G., Bawden L., Brotherton D., Craig S., Cribbes S.,
RA Caplewski L.G., Dexter T.M., Drummond A.H., Gearing A.H.,
RA Heyworth C.M., Lord B.I., McCourt M., Varley P.G., Wood L.M.,
RA Edwards R.M., Lewis P.J.;
RT "BB-10010: an active variant of human macrophage inflammatory protein-
1 alpha with improved pharmaceutical properties.";
RL Blood 86:4400-4408(1995).
RN [7]
RP SEQUENCE OF 27-40 AND 71-83, AND FUNCTION.
RX MEDLINE=96106406; PubMed=8525373;
RA Cocchi F., DeVico A.L., Garzino-Demo A., Arya S.K., Gallo R.C.,
RA Lusso P.;
```

RT "Identification of RANTES, MIP-1 alpha, and MIP-1 beta as the major  
 RT HIV-suppressive factors produced by CD8+ T cells.";   
 RL Science 270:1811-1815(1995).   
 RN [8]   
 RP SEQUENCE OF 27-51, AND IDENTIFICATION OF LD78-ALPHA(4-69).   
 RX PubMed=7537510;   
 RA Bertini R., Luni W., Sozzani S., Bottazzi B., Ruggiero P.,   
 RA Borachi D., Saggiaro D., Chicco-Bianchi L., Proost P., van Damme J.,   
 RA Mantovani A.;   
 RT "Identification of MIP-1 alpha/LD78 as a monocyte chemoattractant   
 RT released by the HTLV-1-transformed cell line MT4.";   
 RL AIDS Res. Hum. Retroviruses 11:155-160(1995).   
 RN [9]   
 RP SUBUNIT, AND INTERACTION WITH MIP-1-BETA(3-69).   
 RX PubMed=12070155; DOI=10.1074/jbc.M203077200.   
 RA Guan E., Wang J., Rodriguez G., Norcross M.A.; CCL4 affects receptor   
 RT "Natural truncation of the chemokine MIP-1beta /CCL4 affects receptor   
 RT specificity but not anti-HIV-1 activity.";   
 RL J. Biol. Chem. 277:32348-32352(2002).   
 RN [10]   
 RP REVIEW   
 RX PubMed=12401480; DOI=10.1016/S1359-6101(02)00045-X;   
 RA Menten P., Wuyts A., Van Damme J.;   
 RT "Macrophage inflammatory protein-1.";   
 RL Cytokine Growth Factor Rev. 13:455-481(2002).   
 RN [11]   
 RP STRUCTURE OF 24-92 BY NMR, AND MUTAGENESIS OF ASP-49 AND GLU-89.   
 RX PubMed=10347159; DOI=10.1074/jbc.274.23.16077;   
 RA Czaplewski L.G., McKeating J., Craven C.J., Higgins L.D., Appay V.,   
 RA Brown A., Dudgeon T., Howard L.A., Meyers T., Owen J., Palan S.R.,   
 RA Tan P., Wilson G., Woods N.R., Heyworth C.M., Lord B.I.,   
 RA Brotherton D., Christison R., Craig S., Cribbes S., Edwards R.M.,   
 RA Evans S.J., Gilbert R., Morgan P., Elliot Randle E., Schofield N.,   
 RA Varley P.G., Fisher J., Jonathan P., Waltho J.P., Hunter M.G.;   
 RT "Identification of amino acid residues critical for aggregation of   
 RT human CC chemokines macrophage inflammatory protein (MIP)-1alpha, MIP-   
 RT 1beta, and RANTES. Characterization of active disassembled chemokine   
 RT variants.";   
 RL J. Biol. Chem. 274:16077-16084(1999).   
 CC -I- FUNCTION: Monokine with inflammatory and chemokinetic properties.   
 CC Binds to CCR1, CCR4 and CCR5. One of the major HIV-suppressive   
 CC factors produced by CD8+ T cells. Recombinant MIP-1-alpha induces   
 CC a dose-dependent inhibition of different strains of HIV-1, HIV-2,   
 CC and simian immunodeficiency virus (SIV).   
 CC -I- SUBUNIT: Self-associates. Also heterodimer of MIP-1-alpha(4-69)   
 CC and MIP-1-beta(3-69).   
 CC -I- SUBCELLULAR LOCATION: Secreted.   
 CC -I- INDUCTION: By TPA or PHA (TPA = 12-o-tetradecanoyl phorbol-13   
 CC acetate (tumor promoter); PHA = phytohemagglutinin (T-cell   
 CC mitogen)).   
 CC -I- PTM: N-terminal processed form LD78-alpha(4-69) is produced by   
 CC proteolytic cleavage after secretion from HTLV1-transformed T-   
 CC cells.   
 CC -I- SIMILARITY: Belongs to the intercrine beta (chemokine CC) family.   
 CC -----   
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 CC -----   
 DR EMBL; D00044; BAA00029.1; -;   
 DR EMBL; M23452; AAA36316.1; -;   
 DR EMBL; M25315; AAA57255.1; -;   
 DR EMBL; X03754; CAA27388.1; -;   
 DR EMBL; X04018; CAA27643.1; ALT\_SEQ.   
 DR EMBL; M23178; AAA35858.1; -;   
 DR EMBL; D90144; BAA14172.1; -;   
 DR EMBL; AF043339; AAC03539.1; -;   
 DR PIR; A35673; A30574.   
 DR PDB; 1B50; NMR; A/B=24-92.

DR PDB; 1B53; NMR; A/B=24-92.   
 DR Genew; HGNC:10627; CCL3.   
 DR MIM; 182283; -; C-soluble fraction; TAS.   
 DR GO; GO:0005625; -; C-soluble fraction; TAS.   
 DR GO; GO:0008009; F:chemokine activity; TAS.   
 DR GO; GO:0004871; F:signal transducer activity; TAS.   
 DR GO; GO:0019735; P:antimicrobial humoral response (sensu Verte. . .; TAS.   
 DR GO; GO:0006874; P:calcium ion homeostasis; TAS.   
 DR GO; GO:0006928; P:cell motility; TAS.   
 DR GO; GO:0007267; P:cell-cell signaling; TAS.   
 DR GO; GO:0006935; P:chemotaxis; TAS.   
 DR GO; GO:0007010; P:cytoskeleton organization and biogenesis; TAS.   
 DR GO; GO:0006887; P:exocytosis; TAS.   
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; TAS.   
 DR GO; GO:0006954; P:inflammatory response; TAS.   
 DR GO; GO:0045069; P:regulation of viral genome replication; TAS.   
 DR GO; GO:0007165; P:signal transduction; TAS.   
 DR InterPro; IPR000827; CC-chemokine\_sml.   
 DR InterPro; IPR001811; Chemokine\_IL8.   
 DR Pfam; PF00048; IL8; 1.   
 DR PROSITE; PS00472; SMALL CYTOKINES CC; 1.   
 KW 3D-structure; Chemotaxis; Cytokine; Direct protein sequencing;   
 KW Inflammatory response; Signal.   
 FT SIGNAL 1 23   
 FT CHAIN 24 92   
 FT CHAIN 27 92   
 FT DISULFID 33 57   
 FT DISULFID 34 73   
 FT MOTAGEN 49 49   
 FT MUTAGEN 89 89   
 FT TURN 44 46   
 FT STRAND 49 51   
 FT TURN 55 58   
 FT STRAND 63 65   
 FT TURN 67 68   
 FT TURN 76 77   
 FT HELIX 79 84   
 FT TURN 85 88   
 SQ SEQUENCE 92 AA; 10085 MW; 517865D5D6776CA8 CRC64;   
 Query Match 7.5%; Score 7; DB 1; Length 92;   
 Best Local Similarity 100.0%; Pred. No. 22;   
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;   
 QY 57 SQCSKPG 63   
 DB 55 SQCSKPG 61   
 RESULT 16   
 Q9MG95 PRELIMINARY; PRT; 92 AA.   
 AC Q9MG95;   
 DT 01-OCT-2000 (TEMBLrel. 15, Created)   
 DT 01-OCT-2000 (TEMBLrel. 15, Last sequence update)   
 DT 01-JUN-2003 (TEMBLrel. 24, Last annotation update)   
 DE Ribosomal protein S19.   
 GN Names=rpS19;   
 OS Chrysodidymus synuroides.   
 OG Mitochondrion.   
 OC Eukaryota; stramenopiles; Chrysophyceae; Synurales; Chrysodidymus.   
 OX NCBI\_TaxID=47573;   
 RN [1]   
 RP SEQUENCE FROM N.A.   
 RX MEDLINE=20330374; PubMed=10871400; DOI=10.1093/nar/28.13.2512;   
 RA Chesnick J.M., Goff M., Graham J., Ocampo C., Lang B.F., Seif E.,   
 RA Burger G.;   
 RT "The mitochondrial genome of the stramenopile alga Chrysodidymus   
 RT synuroides. Complete sequence, gene content and genome   
 RT organization.";   
 RL Nucleic Acids Res. 28:2512-2518(2000).



```

CC -!- SIMILARITY: Belongs to the S19P family of ribosomal proteins.
DR EMBL; AF222716; AAF36954.1; -.
DR HSP; P80381; IQPF.
DR GO; GO:0005739; C:Mitochondrion; IEA.
DR GO; GO:0005840; C:ribosome; IEA.
DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
DR GO; GO:0006412; P:protein biosynthesis; IEA.
DR InterPro; IPR002222; Ribosomal_S19.
DR Pfam; PF00203; Ribosomal_S19; 1.
DR PRINTS; PR00975; RIBOSOMALS19.
DR PRODOM; PD01012; Ribosomal_S19; 1.
DR PROSITE; PS00323; RIBOSOMAL_S19; 1.
KW Mitochondrion; Ribonucleoprotein; Ribosomal protein.
SQ SEQUENCE 92 AA; 11031 MW; 4DDA14117B58C74 CRC64;

Query Match 7.5%; Score 7; DB 2; Length 92;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 AIPFLL 13
DB 34 AIPFLL 40

RESULT 17
ID -SY03_BOVIN STANDARD; PRT; 93 AA.
AC Q8SQA6;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Small inducible cytokine A3 precursor (CCL3) (Macrophage inflammatory
DE protein 1-alpha) (MIP-1-alpha).
GN Name=CCL3; Synonyms=SCYA3;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
[1]
RP SEQUENCE FROM N.A.
RA Werling D.;
RT "Role of chemokines in RSV infection.";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
-!- FUNCTION: Monokine with inflammatory and chemokinetic properties.
CC Binds to CCR1, CCR4 and CCR5 (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the intercrine beta (chemokine CC) family.
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or send an email to license@ebi-sib.ch).
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DR EMBL; AY077840; AAL78060.1; -.
DR InterPro; IPR000827; CC_chemokine.sml.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR SMART; SM00199; SCY; 1.
DR PROSITE; PS00472; SMALL_CYTOKINES CC; 1.
DR Chemotaxis; Cytokine; Inflammatory response; Signal.
FT SIGNAL 1 24 By similarity;
FT CHAIN 25 93 Small inducible cytokine A3.
FT DISULFID 34 58 By similarity.
FT DISULFID 35 74 By similarity.
SQ SEQUENCE 93 AA; 10118 MW; 1266BFBFCBE58E9 CRC64;

Query Match 7.5%; Score 7; DB 1; Length 93;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 57 SQCSKPG 63
DB 56 SQCSKPG 62

RESULT 18
Q6DUK4
ID Q6DUK4 PRELIMINARY; PRT; 93 AA.
AC Q6DUK4;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Macrophage inflammatory protein 1 alpha.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
[1]
RP SEQUENCE FROM N.A.
RA Stirling C.M.A.; Takamatsu H.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY643423; AAT65077.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008009; F:chemokine activity; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR000827; CC_chemokine.sml.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR SMART; SM00199; SCY; 1.
DR PROSITE; PS00472; SMALL_CYTOKINES CC; 1.
SQ SEQUENCE 93 AA; 10117 MW; 0B8D26CABE28414C CRC64;

Query Match 7.5%; Score 7; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 57 SQCSKPG 63
DB 56 SQCSKPG 62

RESULT 19
Q6ESX0
ID Q6ESX0 PRELIMINARY; PRT; 115 AA.
AC Q6ESX0;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE NADH dehydrogenase subunit 3.
GN Name=nad3;
OS Diplometopon zarudnyi (Zarudnyi's worm lizard).
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Amphisbaenia; Trogonophidae;
OC Diplometopon.
OX NCBI_TaxID=94420;
[1]
RP SEQUENCE FROM N.A.
RX PubMed=15324836; DOI=10.1016/j.ympev.2004.05.003;
RA Macey J.R.; Papenfuss T.J.; Kuehl J.V.; Fourcade H.M.; Boore J.L.;
RT "Phylogenetic relationships among amphisbaenian reptiles based on
RT complete mitochondrial genomic sequences.";
RL Mol. Phylogenet. Evol. 33:22-31(2004).
CC -!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
CC -!- SIMILARITY: Belongs to the complex I subunit 3 family.
DR EMBL; AY605474; AAT08510.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
DR InterPro; IPR000440; Oxidored q4.
DR Pfam; PF00507; Oxidored q4; 1.
DR Mitochondrion; NAD; Oxidoreductase; Ubiquinone.
KW Mitochondrion; NAD; Oxidoreductase; Ubiquinone.
SQ SEQUENCE 115 AA; 13186 MW; 088A852664ABFE01 CRC64;

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Query Match      7.5%; Score 7; DB 2; Length 115;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 LLTITAL 18
DB 11 LLTITAL 17

RESULT 20
Q85D00 PRELIMINARY; PRT; 116 AA.
AC Q85D00;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE NADH dehydrogenase subunit 3.
GN Name=ND3;
OS Platyroctes apus (legless searid).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Argentiniformes; Platyroctidae; Platyroctes.
OX NCBI_TaxID=170202;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22628593; PubMed=12742752; DOI=10.1016/S1055-7903(02)00418-9;
RA Ishiguro N.B., Miya M., Nishida M.;
RT "Basal euteleostean relationships: a mitogenomic perspective on the
RT phylogenetic reality of the "protacanthopterygii";
RL Mol. Phylogenet. Evol. 27:476-488(2003).
CC -1- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
CC -1- SIMILARITY: Belongs to the complex I subunit 3 family.
DR EMBL; AP004107; BAC58219.1; .
DR GO; GO:0005739; C:mitochondrion; IEA.
DR GO; GO:0008137; F:NADH dehydrogenase (ubiquinone) activity; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006120; P:mitochondrial electron transport, NADH to u. . .; IEA.
DR InterPro; IPR000440; Oxidored_q4.
DR Pfam; PF00507; Oxidored_q4_1.
KW Mitochondrion; NAD; Oxidoreductase; Ubiquinone.
SQ SEQUENCE 116 AA; 12920 MW; 63250CB6F286F276 CRC64;

Query Match      7.5%; Score 7; DB 2; Length 116;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 LLTITAL 18
DB 8 LLTITAL 14

RESULT 21
Q8LX58 PRELIMINARY; PRT; 118 AA.
AC Q8LX58;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE NADH3 protein.
GN Name=nadh3;
OS Cynocephalus variegatus (Flying lemur).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Dermoptera; Cynocephalidae; Cynocephalus.
OX NCBI_TaxID=9457;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22056029; PubMed=12034869; DOI=10.1073/pnas.102164299;
RA Arnason U., Adegoke J.A., Bodin K., Born E.W., Esa Y.B., Gullberg A.,
RA Nilsson M., Short R.V., Xu X., Janke A.;
RT "Mammalian mitogenomic relationships and the root of the eutherian
RT tree.";

Proc. Natl. Acad. Sci. U.S.A. 99:8151-8156(2002).
-1- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
CC -1- SIMILARITY: Belongs to the complex I subunit 3 family.
DR EMBL; AJ428849; CAD21800.2; .
DR GO; GO:0005739; C:mitochondrion; IEA.
DR GO; GO:0008137; F:NADH dehydrogenase (ubiquinone) activity; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006120; P:mitochondrial electron transport, NADH to u. . .; IEA.
DR InterPro; IPR000440; Oxidored_q4.
DR Pfam; PF00507; Oxidored_q4_1.
KW Mitochondrion; NAD; Oxidoreductase; Ubiquinone.
SQ SEQUENCE 118 AA; 13382 MW; F6FE57203218C19 CRC64;

Query Match      7.5%; Score 7; DB 2; Length 118;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 LLTITAL 18
DB 16 LLTITAL 22

RESULT 22
SY02_CAVPO STANDARD; PRT; 120 AA.
AC Q08782;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Small inducible cytokine A2 precursor (CCl2) (Monocyte chemotactic
DE protein 1) (MCP-1) (Monocyte chemoattractant protein-1).
GN Name=CCl2; Synonyms=MCPI, SCYA2;
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Z; TISSUE=Spleen;
RX MEDLINE=93267104; PubMed=8496603;
RX Yoshimura T.;
RA "cDNA cloning of guinea pig monocyte chemoattractant protein-1 and
RT expression of the recombinant protein.";
RL J. Immunol. 150:5025-5032(1993).
CC -1- FUNCTION: Chemotactic factor that attracts monocytes, but not
CC neutrophils.
CC -1- SUBUNIT: Monomer or homodimer; in equilibrium (By similarity).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the interleukin beta (chemokine CC) family.
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DR EMBL; L04985; AAA37047.1; .
DR FIP; I48147; I48147.
DR HSSP; P80099; 1B00.
DR InterPro; IPR000827; CC_chemokine_sm1.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR SMART; SM00199; SCY; 1.
DR PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
KW Chemotaxis; Cytokine; Glycoprotein; Inflammatory response;
KW Pyrrolidone carboxylic acid; Signal.
FT SIGNAL 1 23 By similarity.
FT CHAIN 24 120 Small inducible cytokine A2.
FT MOD_RES 24 24 Pyrrolidone carboxylic acid (By
FT similarity).
FT DISULFID 33 57 By similarity.
```

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FT DISULFID 34 73 BY similarity.
ET CARBOHYD 97 97 M-linked (GLCNAC... ) (Potential).
SQ SEQUENCE 120 AA; 13741 MW; 5905596851CFC1C54 CRC64;

Query Match
Best Local Similarity 100.0%; Pred. No. 27; Length 120;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 81 KWQDYI 87
Db 79 KWQDYI 85

RESULT 23
RSD_SALTY STANDARD; PRT; 162 AA.
AC Q9L9I6;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Regulator of sigma D.
GN Name=rsd; OrderedLocusNames=STM4165; ORFNames=STM4165;
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=602;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LT2 / ATCC 700720;
RX MEDLINE=21534948; PubMed=11677609; DOI=10.1038/35101614;
RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA Ryan E., Sun H., Flores L., Miller W., Stoneking T., Nhan M.,
RA Waterston R., Wilson R.K.;
RA "Complete genome sequence of Salmonella enterica serovar Typhimurium
RT LT2.";
RL Nature 413:852-856(2001).
CC -!- FUNCTION: Has binding activity to the major sigma subunit of RNA
CC polymerase. May be involved in replacement of the RNA polymerase
CC sigma subunit from sigma-70 to sigma-S during the transition from
CC exponential growth to the stationary phase (By similarity).
CC -!- SIMILARITY: Belongs to the rsd/algQ family.
CC -----
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CC -----
DR EMBL; AF170176; AAF33507.1; -
DR EMBL; AE008894; AAL22993.1; -
DR PDB; 1LJA; Model; A-3-155.
DR StyGene; SG7777; red.
DR InterPro; IPR007448; Rsd AlgQ.
DR Pfam; PF04353; Rsd AlgQ; 1.
KW 3D-structure; Complete proteome; Transcription regulation.
SQ SEQUENCE 162 AA; 18653 MW; 60A52C4D9B0142D8 CRC64;

Query Match
Best Local Similarity 100.0%; Pred. No. 34; Length 162;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 47 QRIMDYI 53
Db 101 QRIMDYI 107

RESULT 24
Q82327 PRELIMINARY; PRT; 162 AA.
ID Q82327
```

```
AC Q8Z327; Q7C6P6;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Putative regulatory protein.
GN Name=rsd; OrderedLocusNames=STY3720, t3466;
OS Salmonella typhi.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=601;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CT18;
RX MEDLINE=21534947; PubMed=11677608; DOI=10.1038/35101607;
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
RA Churcher C.M., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia M.,
RA Baker S., Basham D., Brooks K., Chillingworth T., Connetton P.,
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
RA Quail M.A., Rutherford K.M., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrall B.G.;
RA "Complete genome sequence of a multiple drug resistant Salmonella
RT enterica serovar Typhi CT18.";
RL Nature 413:848-852(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=TY2 / ATCC 700931;
RX MEDLINE=22531367; PubMed=12644504;
RX DOI=10.1128/JB.185.7.2330-2337.2003;
RA Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
RA Burland V., Kodyonni V., Schwartz D.C., Blattner F.R.;
RA "Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
RT and CT18.";
RL Bacteriol. 185:2330-2337(2003).
DR EMBL; AL627279; CAD09479.1; -
DR EMBL; AE016845; AAO70982.1; -
DR GO; GO:0030528; F:transcription regulator activity; IEA.
DR GO; GO:0045449; P:regulation of transcription; IEA.
DR Pfam; PF04353; Rsd AlgQ; 1.
KW Complete proteome.
SQ SEQUENCE 162 AA; 18683 MW; A2CFCFB82A8842C0 CRC64;

Query Match
Best Local Similarity 100.0%; Pred. No. 34; Length 162;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 47 QRIMDYI 53
Db 101 QRIMDYI 107

RESULT 25
Q7RU57 PRELIMINARY; PRT; 214 AA.
ID Q7RU57
AC Q7RU57;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein BL2FI.130.
GN Name=NCU03449.1;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OR74A;
RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
RA Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,
RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
RA Qui D., Iankiev P., Pedersen D., Nelson M., Washburne M., Schulte U.,
RA Selitrennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
```

RA Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,  
RA Roy A., Foley K., Naylor J., Thomann N., Bartlett R., Gnerre S.,  
RA Kamal M., Kanvesselis M., Mauceli E., Bielek C., Rudd S., Frishman D.,  
RA Kryzofova S., Rasmussen C., Merzenberg R.L., Perkins D.D., Kroken S.,  
RA Cogoni C., Macino G., Catchside D., Li W., Pratt R.J., Osmari S.A.,  
RA DeSouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,  
RA Varden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,  
RA Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M.,  
RA Paulsen I., Sachs M.S., Lander E.S., Nusbaum C., Birren B.,  
RT "The Genome Sequence of the Filamentous Fungus Neurospora crassa.";  
RL Nature 0:0-0(2003).  
CC -1- CAUTION: The sequence shown here is derived from an  
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
CC preliminary data.  
CC ENBL; AABX01000737; EAA27499.1; -.  
DR InterPro; IPR001254; Peptidase\_S1.  
DR PROSITE; PS00134; TRYPSIN\_HIS; UNKNOWN\_1.  
KW Hypothetical protein.  
SQ SEQUENCE 214 AA; 23078 MW; B3269D4996764AC0 CRC64;  
  
Query Match 7.5%; Score 7; DB 2; Length 214;  
Best Local Similarity 100.0%; Pred. No. 42;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 22 TESSRG 28  
Db 14 TESSRG 20  
|||||  
  
RESULT 26  
Q8EPK2 PRELIMINARY; PRT; 221 AA.  
AC Q8EPK2;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE ABC transporter permease.  
GN OrderedLocustNames=OB2099;  
OS Oceanobacillus iheyensis.  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Oceanobacillus.  
OX NCBI\_TaxID=182710;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=HTE831;  
RX MEDLINE=2220767; PubMed=12235376; DOI=10.1093/nar/gkf526;  
RA Takami H., Takaki Y., Uchiyama I.;  
RT "Genome sequence of Oceanobacillus iheyensis isolated from the Iheya  
RT Ridge and its unexpected adaptive capabilities to extreme  
RT environments.";  
RL Nucleic Acids Res. 30:3927-3935(2002).  
CC -1- FUNCTION: Part of a binding-protein-dependent transport system.  
CC Probably responsible for the translocation of the substrate across  
CC the membrane (By similarity).  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).  
CC -1- SIMILARITY: Belongs to the binding-protein-dependent transport  
CC system permease family.  
CC ENBL; AP004600; BAC14055.1; -.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0005215; F:transporter activity; IEA.  
DR GO; GO:0006810; P:transport; IEA.  
DR InterPro; IPR006140; 2-Hacid\_DH\_C.  
DR InterPro; IPR000515; BPD\_transp\_1.  
DR Pfam; PF00528; BPD\_transp\_1; 1.  
DR PROSITE; PS00928; ABC\_TM1; 1.  
DR PROSITE; PS00065; D\_2\_HYDROXYACID\_DH\_1; UNKNOWN\_1.  
KW Complete proteome; Transmembrane; Transport.  
SQ SEQUENCE 221 AA; 23972 MW; 4C0463264425855 CRC64;  
  
Query Match 7.5%; Score 7; DB 2; Length 221;  
Best Local Similarity 100.0%; Pred. No. 43;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 4 SVAAI PF 10

Db 101 SVAAI PF 107  
|||||  
  
RESULT 27  
HXK6\_HUMAN STANDARD; PRT; 235 AA.  
AC P09630;  
DT 01-MAR-1989 (Rel. 10, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Homeobox protein Hox-C6 (Hox-3C) (HHO.C8) (CP25).  
GN Name=HOXC6; Synonyms=HOX3C;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RX MEDLINE=87260899; PubMed=2885844;  
RA Simeone A., Mavilio F., Acampora D., Giampaolo A., Faiella A.,  
RA Zappavigna V., D'Esposito M., Pannese M., Russo G., Boncinelli E.,  
RA Peschle C.;  
RT "Two human homeobox genes, c1 and c8: structure analysis and  
RT expression in embryonic development.";  
RL Proc. Natl. Acad. Sci. U.S.A. 84:4914-4918(1987).  
RN [2]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RX MEDLINE=88262550; PubMed=2898768;  
RA Simeone A., Pannese M., Acampora D., D'Esposito M., Boncinelli E.;  
RT "At least three human homeoboxes on chromosome 12 belong to the same  
RT transcription unit.";  
RL Nucleic Acids Res. 16:5379-5390(1988).  
RN [3]  
RP SEQUENCE FROM N.A. (ISOFORM 2).  
RX MEDLINE=97024425; PubMed=8870653;  
RA Chariot A., Castronovo V., Le P., Gillet C., Sobel M.E., Gielen J.;  
RT "Cloning and expression of a new HOXC6 transcript encoding a  
RT repressing protein.";  
RL Biochem. J. 319:91-97(1996).  
RN [4]  
RP SEQUENCE OF 141-206 FROM N.A.  
RX MEDLINE=90215256; PubMed=2576652;  
RA Boncinelli E., Acampora D., Pannese M., D'Esposito M., Somma R.,  
RA Gaudino G., Stornaiuolo A., Cafiero M., Faiella A., Simeone A.;  
RT "Organization of human class I homeobox genes.";  
RL Genome 31:745-756(1989).  
CC -1- FUNCTION: Sequence-specific transcription factor which is part of  
CC a developmental regulatory system that provides cells with  
CC specific positional identities on the anterior-posterior axis.  
CC -1- SUBCELLULAR LOCATION: Nuclear.  
CC -1- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=2;  
CC Name=1;  
CC IsoId=P09630-1; Sequence=Displayed;  
CC Name=2;  
CC IsoId=P09630-2; Sequence=VSP\_002392;  
CC -1- SIMILARITY: Belongs to the Antp homeobox family.  
CC -1- SIMILARITY: Contains 1 homeobox domain.  
CC -----  
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CC -----  
DR ENBL; S82986; AAB46892.1; -.  
DR ENBL; M16938; AAA36007.1; -.  
DR PIR; B28030; WJHU3C.  
DR HSSP; P02833; 9ANT.  
DR TRANSFAC; T01742; -.



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Query Match      7.5%; Score 7; DB 1; Length 235;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 SSSRGPy 30
Db 64 SSSRGPy 70

RESULT 29
Q8TM45 PRELIMINARY; PRT; 247 AA.
AC Q8TM45;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Predicted protein.
GN OrderedLocNames=MA2825;
OS Methanoscarchina acetivorans.
OC Archaea; Euryarchaeota; Methanomicrobia; Methanoscarchinales;
OC Methanoscarchinaceae; Methanoscarchina.
OX NCBI_TaxID=2214;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C2A / ATCC 35395 / DSM 2834;
RX MEDLINE=21929760; PubMed=11932238; DOI=10.1101/gr.223902;
RA Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P.,
RA FitzHugh W., Calvo S., Engels R., Smirnov S., Atnoor D., Brown A.,
RA Allen N., Naylor J., Stange-Thomann N., Dearellano K., Johnson R.,
RA Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W.,
RA Zimmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guss A.M.,
RA Hedderich R., Ingram-Smith C., Kuetner H.C., Krzycki J.A.,
RA Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,
RA Springer T.A., Umayam L.A., White O., White R.H., de Macario E.C.,
RA Ferry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I.T.,
RA Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,
RA Metcalf W.W., Birren B.;
RT "The genome of Methanoscarchina acetivorans reveals extensive metabolic
RT and physiological diversity.";
RL Genome Res. 12:532-542(2002).
DR EMBL; AE010982; AAM06204.1; -.
KW Complete proteome.
SQ SEQUENCE 247 AA; 28575 MW; 17EFB83302522318 CRC64;

Query Match      7.5%; Score 7; DB 2; Length 247;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 ITIALGT 20
Db 73 ITIALGT 79

RESULT 30
O44332 PRELIMINARY; PRT; 255 AA.
AC O44332;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hemocyte protease-3.
OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Sphingioidea;
OC Spingidae; Sphinginae; Manduca.
OX NCBI_TaxID=7130;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99124363; PubMed=9927173;
RA Jiang H., Wang Y., Kanost M.R.;
RT "Four serine proteinases expressed in Manduca sexta haemocytes.";
RL Insect Mol. Biol. 8:39-53(1999).
CC -|- SIMILARITY: Belongs to peptidase family S1.
```

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OM protein - protein search, using sw model

Run on: September 19, 2005, 08:47:31 ; Search time 174 Seconds  
(without alignments)  
273.697 Million cell updates/sec

Title: US-10-626-530-2

Perfect score: 504

Sequence: 1 MKTSVAIPFLITLITLGT.....VCTNPDKWQDIKDKEN 93

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : UniProt\_03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	504	100.0	93	1 SY14 HUMAN	Q16627 homo sapien
2	258.5	51.3	93	2 Q6DUF4	Q6DUF4 sus scrofa
3	240.5	47.7	93	1 SY3L HUMAN	P16619 homo sapien
4	239	47.4	92	2 Q8HYQ3	Q8HYQ3 macaca mula
5	238.5	47.3	93	1 SY03 BOVIN	Q8QA66 bos taurus
6	237.5	47.1	92	2 Q711P4	Q711P4 sus scrofa
7	236	46.8	92	1 SY03 HUMAN	P10147 h small ind
8	235.5	46.7	90	1 SY04 CHICK	Q90826 gallus gall
9	235.5	46.7	90	2 Q9PWA6	Q9PWA6 gallus gall
10	234.5	46.5	92	1 SY04 MOUSE	P14097 mus musculus
11	230.5	45.7	92	1 SY04 RABIT	P46632 oryctolagus
12	229.5	45.5	92	1 SY04 RAT	P50230 rattus norv
13	229.5	45.5	92	2 Q8HYQ2	Q8HYQ2 macaca mula
14	228.5	45.3	92	2 Q8NHW4	Q8NHW4 homo sapien
15	225.5	44.7	92	1 Q68A20	Q68A20 canis famil
16	224.5	44.5	92	1 SY04 HUMAN	P13236 h small ind
17	223.5	44.3	92	2 Q6NSB0	Q6NSB0 homo sapien
18	223	44.2	92	1 SY03 MOUSE	P10855 mus musculus
19	223	44.2	92	1 SY03 RAT	P50229 rattus norv
20	222.5	44.1	92	2 Q91ZL0	Q91ZL0 sigmodon hi
21	220	43.7	92	2 Q68A92	Q68A92 canis famil
22	217.5	43.2	85	2 Q80XG5	Q80XG5 peromyscus
23	213.5	42.4	80	2 Q14745	Q14745 homo sapien
24	209	41.5	56	2 Q8HYN4	Q8HYN4 macaca mula
25	209	41.5	89	2 Q918E0	Q918E0 gallus gall
26	208	41.3	89	1 SY18 HUMAN	P55774 h small ind
27	201.5	40.0	120	1 SY23 HUMAN	P55773 homo sapien
28	199	39.5	92	2 Q91ZG5	Q91ZG5 sigmodon hi
29	197	39.1	88	2 Q8HYF8	Q8HYF8 macaca mula
30	194.5	38.6	92	1 SY05 RAT	P50231 rattus norv
31	194.5	38.6	92	2 Q6PDI1	Q6PDI1 rattus norv

32	191	37.9	91	1 SY05 HUMAN	P13501 homo sapien
33	189	37.5	91	1 SY05_MOUSE	P13082 mus musculus
34	188	37.3	91	1 SY05_HORSE	Q8MKD0 equus cabal
35	188	37.3	113	1 SY15 HUMAN	Q16663 homo sapien
36	183	36.3	91	1 SY05_CANFA	Q8HYE0 canis famil
37	183	36.3	91	1 SY05_CAVPO	P97272 cavia porce
38	183	36.3	91	2 Q8HYQ1	Q8HYQ1 macaca mula
39	182	36.1	92	1 SY05_FELCA	Q8EQ40 felis silve
40	181.5	36.0	120	1 SY16_HUMAN	Q15467 h small ind
41	180.5	35.8	91	2 Q8QGS7	Q8QGS7 gallus gall
42	180	35.7	116	1 SY06_MOUSE	P27784 mus musculus
43	178.5	35.4	115	2 Q68FP3	Q68FP3 rattus norv
44	177.5	35.2	98	1 SY13_CANFA	Q68Y88 canis famil
45	176	34.9	49	2 Q8HYN3	Q8HYN3 macaca mula
46	176	34.9	101	2 Q64IC2	Q64IC2 oncorhynch
47	175	34.7	91	1 SY05_BOVIN	Q97919 bos taurus
48	175	34.7	91	1 SY05_SIGHI	Q91211 sigmodon hi
49	173.5	34.4	98	1 SY13_HUMAN	Q99616 homo sapien
50	173.5	34.4	116	2 Q6IVB4	Q6IVB4 rattus norv
51	171.5	34.0	101	2 Q8JRS7	Q8JRS7 guinea pig
52	170.5	33.8	119	2 Q8K477	Q8K477 rattus norv
53	168.5	33.4	122	1 SY09_MOUSE	P51670 mus musculus
54	166	32.9	94	2 Q64H35	Q64H35 canis famil
55	163.5	32.4	94	1 SY26_HUMAN	Q9Y258 homo sapien
56	163.5	32.4	101	2 Q672Y4	Q672Y4 ictalurus f
57	163.5	32.4	119	1 SY24_MOUSE	Q5JKC0 mus musculus
58	162.5	32.2	92	1 REG1_BOVIN	P82943 bos taurus
59	162.5	32.2	120	2 Q8HYF4	Q8HYF4 macaca mula
60	162	32.1	79	2 Q672V7	Q672V7 ictalurus p
61	161	31.9	91	2 Q8QGS6	Q8QGS6 gallus gall
62	160	31.7	95	2 Q98158	Q98158 human herpe
63	159	31.5	97	1 EOTA_RAT	P97545 rattus norv
64	157.5	31.2	150	2 Q8CGM5	Q8CGM5 sigmodon hi
65	156	31.0	125	1 SY02_RABIT	P28292 oryctolagus
66	155	30.8	99	1 SY08_HUMAN	P80075 homo sapien
67	153.5	30.5	99	1 SY02_PIG	P42831 sus scrofa
68	153	30.4	91	2 Q8AV56	Q8AV56 paralichthy
69	153	30.4	99	2 Q68AY9	Q68AY9 canis famil
70	152	30.2	99	2 Q8HYQ0	Q8HYQ0 macaca mula
71	152	30.2	99	2 Q8MKC8	Q8MKC8 equus cabal
72	152	30.2	99	2 Q865F4	Q865F4 macaca neme
73	151	30.0	99	1 SY02_HORSE	Q9TTG3 equus cabal
74	151	30.0	99	2 Q95N01	Q95N01 canis famil
75	150.5	29.9	148	1 SY02_MOUSE	P10148 mus musculus
76	150	29.8	50	2 Q8HYN5	Q8HYN5 macaca mula
77	150	29.8	94	1 SY17_HUMAN	Q92583 homo sapien
78	150	29.8	97	1 EOTA_MOUSE	P48298 mus musculus
79	150	29.8	100	1 EOTA_HORSE	Q9TTG4 equus cabal
80	150	29.8	101	1 SY02_CANFA	P52203 canis famil
81	149	29.6	148	1 SY02_RAT	P14844 rattus norv
82	148.5	29.5	99	1 MCPA_BOVIN	P28291 bos taurus
83	148	29.4	99	1 SY08_BOVIN	Q09141 bos taurus
84	147	29.2	91	2 Q8JIM4	Q8JIM4 paralichthy
85	146	29.0	91	2 Q8JIM5	Q8JIM5 paralichthy
86	146	29.0	94	1 WM12_HVH8	Q98157 human herpe
87	146	29.0	97	1 EOTA_HUMAN	P51671 homo sapien
88	146	29.0	99	1 SY07_HUMAN	P80098 homo sapien
89	146	29.0	109	2 Q727Q8	Q727Q8 homo sapien
90	144.5	28.7	119	1 SY24_HUMAN	Q00175 homo sapien
91	144	28.6	99	1 SY08_PIG	P49873 sus scrofa
92	142	28.2	93	2 Q9ERE0	Q9ERE0 rattus norv
93	142	28.2	97	2 Q8HXZ5	Q8HXZ5 macaca mula
94	141	28.0	93	1 SY22_HUMAN	Q00636 homo sapien
95	141	28.0	99	2 Q672X6	Q672X6 ictalurus p
96	141	28.0	109	2 Q865F3	Q865F3 macaca neme
97	139	27.6	94	2 Q8HYF9	Q8HYF9 macaca mula
98	139	27.6	99	2 Q8I021	Q8I021 felis silve
99	138	27.4	131	2 Q9R043	Q9R043 mus musculus
100	137	27.2	74	1 MCPB_BOVIN	P80343 bos taurus

ALIGNMENTS

RESULT 1  
SY14 HUMAN STANDARD; PRT; 93 AA.  
ID \_SY14\_HUMAN  
AC Q16627; Q13954;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Small inducible cytokine A14 precursor (CCL14) (Chemokine CC-1(CC-3)  
DE (HCC-1/HCC-3) (HCC-1(1-74)) (NCC-2) [Contains: HCC-1(3-74); HCC-1(4-  
DE 74); HCC-1(9-74)].  
GN Name=CCL14; Synonyms=NCC2, SCYA14;  
OS Homo sapiens (Human)  
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
[1]  
RN SEQUENCE FROM N.A., AND SEQUENCE OF 20-93.  
RC TISSUE=Bone marrow;  
RX MEDLINE=96136773; PubMed=8551235;  
RA Schulz-Knappe P., Maegert H.-J., Dewald B., Meyer M., Cetin Y.,  
RA Kubbes M., Tomeczkowski J., Kirchhoff K., Raida M., Adermann K.,  
RA Kist A., Reinecke M., Sillard R., Pardigol A., Ugucioni M.,  
RA Baggolini M., Forssmann W.-G.;  
RT "HCC-1, a novel chemokine from human plasma.";  
RL J. Exp. Med. 183:295-299(1996).  
[2]  
RN SEQUENCE FROM N.A.  
RC TISSUE=Liver;  
RX MEDLINE=98263352; PubMed=9600961; DOI=10.1073/pnas.95.11.6308;  
RA Pardigol A., Forssmann U., Zucht H.-D., Loetscher P.,  
RA Schulz-Knappe P., Baggolini M., Forssmann W.-G., Maegert H.-J.;  
RT "HCC-2, a human chemokine: gene structure, expression pattern, and  
RT biological activity.";  
RL Proc. Natl. Acad. Sci. U.S.A. 95:6308-6313(1998).  
[3]  
RN SEQUENCE FROM N.A.  
RC TISSUE=Liver;  
RX MEDLINE=99228475; PubMed=10213461; DOI=10.1089/10799099314153;  
RA Noniyama H., Fukuda S., Ito M., Tanase S., Miura R., Yoshie O.;  
RT "Organization of the chemokine gene cluster on human chromosome  
RT 17q11.2 containing the genes for CC chemokine MIP1-1, HCC-2, LEC, and  
RT RANTES";  
RN J. Interferon Cytokine Res. 19:227-234(1999).  
[4]  
RN SEQUENCE FROM N.A. (ISOFORM HCC-1).  
RC TISSUE=Pancreas, and Spleen;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Dratchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Uesdin T.B., Toehiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J.J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
[5]  
RN SEQUENCE OF 20-32, IDENTIFICATION OF HCC-1(3-74) AND HCC-1(4-74), MASS  
RN SPECTROMETRY, AND CARBOHYDRATE-LINKAGE SITE SER-26.  
RX PubMed=10978165; DOI=10.1021/bi992488q;  
RA Richter R., Schulz-Knappe P., John H., Forssmann W.-G.;  
RT "Posttranslationally processed forms of the human chemokine HCC-1.";

Biochemistry 39:10799-10805(2000).  
[6]  
RN SEQUENCE OF 20-48, IDENTIFICATION OF HCC-1(9-74), MASS SPECTROMETRY,  
RN AND FUNCTION.  
RX PubMed=11085751;  
RA Dethoux M., Staendker L., Vakili J., Muench J., Forssmann U.,  
RA Adermann K., Poehlmann S., Vassart G., Kirchhoff F., Parmentier M.,  
RA Forssmann W.-G.;  
RT "Natural proteolytic processing of hemofiltrate CC chemokine 1  
RT generates a potent CC chemokine receptor (CCR)1 and CCR5 agonist with  
RT anti-HIV properties";  
RL J. Exp. Med. 192:1051-1058(2000).  
CC -I- FUNCTION: Has weak activities on human monocytes and acts via  
CC receptors that also recognize MIP-1 alpha. It induced  
CC intracellular Ca(2+) changes and enzyme release, but no  
CC chemotaxis, at concentrations of 100-1,000 nM, and was inactive on  
CC T lymphocytes, neutrophils, and eosinophil leukocytes. Enhances  
CC the proliferation of CD34 myeloid progenitor cells. The processed  
CC form HCC-1(9-74) is a chemotactic factor that attracts monocytes  
CC eosinophils, and T-cells and is a ligand for CCR1, CCR3 and CCR5.  
CC -I- SUBCELLULAR LOCATION: Secreted.  
CC -I- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=2;  
CC Name=HCC-1;  
CC IsoId=Q16627-1; Sequence=Displayed;  
CC Name=HCC-3;  
CC IsoId=Q16627-2; Sequence=VSP\_001060;  
CC -I- TISSUE SPECIFICITY: Expressed constitutively in several normal  
CC tissues: spleen, liver, skeletal and heart muscle, gut, and bone  
CC marrow, present at high concentrations (1-80 nM) in plasma.  
CC -I- PTM: The N-terminal processed forms HCC-1(3-74), HCC-1(4-74) and  
CC HCC-1(9-74) are produced in small amounts by proteolytic cleavage  
CC after secretion in blood.  
CC -I- PTM: HCC-1(1-74), but not HCC-1(3-74) and HCC-1(4-74), is  
CC partially O-glycosylated; the O-linked glycan consists of one Gal-  
CC GalNAc disaccharide, further modified by two N-acetylneuraminic  
CC acids.  
CC -I- SIMILARITY: Belongs to the intercrine beta (chemokine CC) family.  
-----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
-----  
CC EMBL; Z49270; CAA89264.1; -  
DR EMBL; Z70292; CAA94307.1; -  
DR EMBL; Z70293; CAA94309.1; -  
DR EMBL; Z49269; CAA89263.1; -  
DR EMBL; AF088219; AAC63329.1; -  
DR EMBL; AF088219; AAF23982.1; -  
DR EMBL; BC045165; AAF45165.1; -  
DR HSSP; P13236; LHUM.  
DR Genew; HGNC:10612; CCL14.  
DR MTM; 601392; -  
DR GO; GO:0005615; C:extracellular space; TAS.  
DR GO; GO:0004871; F:signal transducer activity; TAS.  
DR GO; GO:0006874; P:calcium ion homeostasis; TAS.  
DR GO; GO:0006284; P:positive regulation of cell proliferation; TAS.  
DR InterPro; IPR000827; CC chemokine sml.  
DR InterPro; IPR001811; Chemokine\_IL8.  
DR Pfam; PF00048; IL8; 1.  
DR PROSITE; PS00472; SMALL\_CYTOKINES\_CC; 1.  
KW Alternative splicing; Cytokine; Direct protein sequencing;  
KW Glycoprotein; Signal.  
FT SIGNAL 1 19  
FT CHAIN 20 93 Small inducible cytokine A14.  
FT CHAIN 22 93 HCC-1(3-74).  
FT CHAIN 23 93 HCC-1(4-74).  
FT CHAIN 28 93 HCC-1(9-74).  
FT DISULFID 35 59 By similarity.



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FT DISULPID 36 75 By similarity.
FT CARBOHYD 26 26 O-linked (GalNAc...).
FT VARSPLIC 27 27 R -> QTGGKPKVVKIQLKLVG (in isoform HCC-
FT 3).
FT FTID=VSP_001060.
SQ SEQUENCE 93 AA; 10678 MW; DDDDB899DC9148836 CRC64;

Query Match 100.0%; Score 504; DB 1; Length 93;
Best Local Similarity 100.0%; Pred. No. 1e-49;
Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKISVAAPFLLITIALGKTKSSSRGPHVPSGCCFTYTKIPRORIMDYVETNSQCS 60
Db 1 MKISVAAPFLLITIALGKTKSSSRGPHVPSGCCFTYTKIPRORIMDYVETNSQCS 60

Qy 61 KPGIVFTIKRGHSGVCTNPSPDKVQDYIKDMKEN 93
Db 61 KPGIVFTIKRGHSGVCTNPSPDKVQDYIKDMKEN 93

RESULT 2
Q6DUK4 PRELIMINARY; PRT; 93 AA.
AC Q6DUK4
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Macrophage inflammatory protein 1 alpha.
OS Sus scrofa [pig].
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Stirling C.M.A., Takamatsu H.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY643423; AAT65077.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008009; F:chemokine activity; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR000827; CC chemokine sm1.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR SMART; SM00199; SCV; 1.
DR PROSITE; PS00472; SMALL_CYTOKINES CC; 1.
SQ SEQUENCE 93 AA; 10117 MW; 0B8D26CABE28414C CRC64;

Query Match 51.3%; Score 258.5; DB 2; Length 93;
Best Local Similarity 49.5%; Pred. No. 1.2e-21;
Matches 46; Conservative 22; Mismatches 24; Indels 1; Gaps 1;

Qy 1 MKISVAAPFLLITIALGKTKSSSRGPHVPSGCCFTYTKIPRORIMDYVETNSQCS 60
Db 1 MKVAVALA-ILLCAMALCSQVPSAPLGATPTACCFYSYRQLPRKFVADYETSSQCS 59

Qy 61 KPGIVFTIKRGHSGVCTNPSPDKVQDYIKDMKEN 93
Db 60 KPGVIFQTKGKGVCANPDADWQVEYISDLELN 92

RESULT 3
SY3L_HUMAN STANDARD; PRT; 93 AA.
ID SY3L_HUMAN
AC P16619; O96168;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Small inducible cytokine A3 like 1 precursor (Tonsillar lymphocyte
DE LD78 beta protein) (LD78-beta(1-70)) (GO/G1 switch regulatory protein
DE 19-2) (GOS19-2 protein) (PAT 464.2) (Contains: LD78-beta(3-70); LD78-
DE beta(5-70)).
GN Names=CCIL3L1; Synonyms=GOS19-2, SCYA3L1;
OS Homo sapiens (Human).
```

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Irving S.G., Zipfel P.F., Baile J., McBride O.W., Morton C.C.,
RX MEDLINE=90287702; PubMed=1972563;
RA Burd P.R., Siebenlist U., Kelly K.;
RT "Two inflammatory mediator cytokine genes are closely linked and
RT variably amplified on chromosome 17q.";
RL Nucleic Acids Res. 18:3261-3270(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=91103879; PubMed=22711120;
RA Blum S., Forsdyke R.E., Forsdyke D.R.;
RT "Three human homologs of a murine gene encoding an inhibitor of stem
RT cell proliferation.";
RL DNA Cell Biol. 9:589-602(1990).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=90287155; PubMed=1694014;
RA Nakao M., Nomiya H., Shimada K.;
RT "Structures of human genes coding for cytokine LD78 and their
RT expression.";
RL Mol. Cell. Biol. 10:3646-3658(1990).
RN [4]
RP SEQUENCE FROM N.A.
RX TISSUE=B-cell, Pancreas, and Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin I.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [5]
RP SEQUENCE OF 24-38.
RX PubMed=15340161; DOI=10.1110/ps.04682504;
RA Zhang Z., Henzel W.J.;
RT "Signal peptide prediction based on analysis of experimentally
RT verified cleavage sites.";
RL Protein Sci. 13:2819-2824(2004).
RN [6]
RP IDENTIFICATION OF LD78-BETA(3-70) AND LD78-BETA(5-70), N-TERMINAL
RP PROCESSING, AND FUNCTION.
RX PubMed=10961862;
RA Van Damme J.;
RA Proost P., Menten P., Struyf S., Schutyser E., De Meester I.,
RT "Cleavage by CD26/dipeptidyl peptidase IV converts the chemokine
RT LD78beta into a most efficient monocyte attractant and CCRI agonist.";
RL Blood 96:1674-1680(2000).
CC -1- FUNCTION: Chemotactic for monocytes. Is a ligand for CCR5.
CC Recombinant small inducible cytokine B10 induces a dose-dependent
CC inhibition of macrophage tropic HIV-1 strains. The processed form
CC LD78-beta(3-70) shows a 20-fold to 30-fold higher chemotactic
CC activity and is also a ligand for CCRI.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- PTM: The N-terminal processed forms LD78-beta(3-70) and LD78-
```

```
CC beta(5-70) are produced by proteolytic cleavage after secretion
CC from peripheral blood monocytes. The cleavage to yield LD78-
CC beta(3-70) is probably achieved by DP4.
CC -I- SIMILARITY: Belongs to the intercrine beta (chemokine CC) family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X52149; CAA36397.1; -
DR EMBL; M24110; AAA35859.1; -
DR EMBL; D90145; EBA14173.1; -
DR EMBL; BC007783; AAH07783.1; -
DR EMBL; BC027888; AAH27888.1; -
DR PIR; B35673; B35673.
DR HSSP; P10147; IB50.
DR Genew; HGNC:10628; CCL3L1.
DR H-InvDB; HIX0020418; -
DR H-InvDB; HIX0023281; -
DR MIM; 601395; -
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0008009; F:chemokine activity; NAS.
DR GO; GO:0006935; P:chemotaxis; NAS.
DR GO; GO:0006954; P:inflammatory response; TAS.
DR GO; GO:0008285; P:negative regulation of cell proliferation; TAS.
DR InterPro; IPR000827; CC_chemokine_sml.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR SMART; SM00199; SCY; 1.
DR PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
DR Chemotaxis; Cytokine; Direct protein sequencing; Signal.
KW SIGNAL
FT CHAIN 24 93 Small inducible cytokine A3 like 1.
FT CHAIN 26 93 LD78-beta(3-70).
FT CHAIN 28 93 LD78-beta(5-70).
FT SITE 25 26 Cleavage (by DP4) (Probable).
FT DISULFID 34 58 By similarity.
FT DISULFID 35 74 By similarity.
FT CONFLICT 91 91 L -> P (in Ref. 4; AAH07783).
SQ SEQUENCE 93 AA; 10161 MW; A7A79E774006D61E CRC64;

Query Match 47.7%; Score 240.5; DB 1; Length 93;
Best Local Similarity 47.3%; Pred. No. 1.4e-19;
Matches 43; Conservative 22; Mismatches 25; Indels 1; Gaps 1;

QY 1 MKISVAAPFLITIALGKTESSRGYPHSECCFTYTYKIPQRIMDYETNSQCS 60
Db 1 MQVSTAALA-VLLCTMALCNQVLSAPLAADPTACCFSYTSRQIPQNFADYFETSSQCS 59

QY 61 KPGIVFTKRGHVSCTNPSDKWQDYIKDMK 91
Db 60 KPSVIFLTRGRQVCA DPSEWQKVYSDLE 90

RESULT 4
ID Q8HYQ3 PRELIMINARY; PRT; 92 AA.
AC Q8HYQ3
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Macaca mulatta (Rhesus macaque).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.

Query Match 47.7%; Score 240.5; DB 1; Length 93;
Best Local Similarity 47.3%; Pred. No. 1.4e-19;
Matches 43; Conservative 22; Mismatches 25; Indels 1; Gaps 1;

QY 1 MKISVAAPFLITIALGKTESSRGYPHSECCFTYTYKIPQRIMDYETNSQCS 60
Db 1 MQVSTAALA-VLLCTMALCNQVLSAPLAADPTACCFSYTSRQIPQNFADYFETSSQCS 59

QY 61 KPGIVFTKRGHVSCTNPSDKWQDYIKDMK 91
Db 60 KPSVIFLTRGRQVCA DPSEWQKVYSDLE 90

RESULT 4
ID Q8HYQ3 PRELIMINARY; PRT; 92 AA.
AC Q8HYQ3
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Macaca mulatta (Rhesus macaque).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.

Query Match 47.7%; Score 240.5; DB 1; Length 93;
Best Local Similarity 47.3%; Pred. No. 1.4e-19;
Matches 43; Conservative 22; Mismatches 25; Indels 1; Gaps 1;

QY 1 MKISVAAPFLITIALGKTESSRGYPHSECCFTYTYKIPQRIMDYETNSQCS 60
Db 1 MQVSTAALA-VLLCTMALCNQVLSAPLAADPTACCFSYTSRQIPQNFADYFETSSQCS 59

QY 61 KPGIVFTKRGHVSCTNPSDKWQDYIKDMK 91
Db 60 KPSVIFLTRGRQVCA DPSEWQKVYSDLE 90

RESULT 4
ID Q8HYQ3 PRELIMINARY; PRT; 92 AA.
AC Q8HYQ3
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Macaca mulatta (Rhesus macaque).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.

Query Match 47.4%; Score 239; DB 2; Length 92;
Best Local Similarity 48.4%; Pred. No. 2e-19;
Matches 44; Conservative 21; Mismatches 24; Indels 2; Gaps 2;

QY 1 MKISVAAPFLITIALGKTESSRGYPHSECCFTYTYKIPQRIMDYETNSQCS 60
Db 1 MQVSTAALA-VLLCTMALCNRI-SATPAADTPTCCFSYISRQIPQNFADYFETNSQCS 58

QY 61 KPGIVFTKRGHVSCTNPSDKWQDYIKDMK 91
Db 59 KPGVIFLTRGRQVCA DPSEWQKVYSDLE 89

RESULT 5
ID SY03_BOVIN STANDARD; PRT; 93 AA.
AC Q8SQA6;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Small inducible cytokine A3 precursor (CCL3) (Macrophage inflammatory
DE protein 1-alpha) (MIP-1-alpha).
GN Name=CCL3; Synonyms=SCYA3;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Werling D.;
RT "Role of chemokines in RSV infection.";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
CC -I- FUNCTION: Monokine with inflammatory and chemokinetic properties.
CC Binds to CCR1, CCR4 and CCR5 [By similarity].
CC -I- SUBCELLULAR LOCATION: Secreted.
CC -I- SIMILARITY: Belongs to the intercrine beta (chemokine CC) family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AY077840; AAL78060.1; -
DR InterPro; IPR000827; CC_chemokine_sml.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR SMART; SM00199; SCY; 1.
DR PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
DR Chemotaxis; Cytokine; Inflammatory response; Signal.
FT SIGNAL 1 24 By similarity.
FT CHAIN 25 93 Small inducible cytokine A3.
```



RX PubMed=12401480; DOI=10.1016/S1359-6101(02)00045-X;  
RA Menten P., Wuyts A., Van Damme J.;  
RT "Macrophage inflammatory protein-1";  
RN Cytokine Growth Factor Rev. 13:455-481(2002).  
[11]  
RP STRUCTURE OF 24-92 BY NMR, AND MUTAGENESIS OF ASP-49 AND GLU-89.  
RX PubMed=10347159; DOI=10.1074/jbc.274.23.16077;  
RA Czaplinski L.G., McKeating J., Craven C.J., Higgins L.D., Appay V.,  
Brown A., Dudgeon T., Howard L.A., Meyers T., Owen J., Palan S.R.,  
Tan P., Wilson G., Woods N.R., Heyworth C.M., Lord B.I.,  
RA Brotherton D., Christison R., Craig S., Cribbes S., Edwards R.M.,  
RA Evans S.J., Gilbert R., Morgan P., Elliot Randle E., Schofield N.,  
RA Varley P.G., Fisher J., Jonathan P., Waltho J.P., Hunter M.G.;  
RT "Identification of amino acid residues critical for aggregation of  
human CC chemokines macrophage inflammatory protein (MIP)-1alpha, MIP-  
RT 1beta, and RANTES. Characterization of active disaggregated chemokine  
RT variants.";  
RL J. Biol. Chem. 274:16077-16084(1999).  
CC -!- FUNCTION: Monokine with inflammatory and chemokinetic properties.  
CC Binds to CCR1, CCR4 and CCR5. One of the major HIV-suppressive  
CC factors produced by CD8+ T cells. Recombinant MIP-1-alpha induces  
CC a dose-dependent inhibition of different strains of HIV-1, HIV-2,  
CC and simian immunodeficiency virus (SIV).  
CC -!- SUBUNIT: Self-associates. Also heterodimer of MIP-1-alpha (4-69)  
CC and MIP-1-beta(3-69).  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- INDUCTION: By TPA or PHA (TPA = 12-o-tetradecanoyl phorbol-13  
CC acetate (tumor promoter); PHA = phytohemagglutinin (T-cell  
CC mitogen)).  
CC -!- PTM: N-terminal processed form LD78-alpha(4-69) is produced by  
CC proteolytic cleavage after secretion from HTLV1-transformed T-  
CC cells.  
CC -!- SIMILARITY: Belongs to the interleukin beta (chemokine CC) family.  
CC  
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CC  
DR EMBL; D00044; BAA00029.1; -;  
DR EMBL; M23452; AAA36316.1; -;  
DR EMBL; M25315; AAA57255.1; -;  
DR EMBL; X03754; CAA27388.1; -;  
DR EMBL; X04019; CAA27643.1; ALT\_SEQ.  
DR EMBL; M23178; AAA35858.1; -;  
DR EMBL; D90144; BAA14172.1; -;  
DR EMBL; AF043339; AAC03539.1; -;  
DR FIR; A35673; A30574.  
DR PDB; 1B50; NMR; A/B=24-92.  
DR PDB; 1B53; NMR; A/B=24-92.  
DR Genew; HGNC:10627; CCL3.  
DR MIM; 182283; -;  
DR GO; GO:0005625; C:soluble fraction; TAS.  
DR GO; GO:0008009; F:chemokine activity; TAS.  
DR GO; GO:0004871; F:signal transducer activity; TAS.  
DR GO; GO:0019735; P:antimicrobial humoral response (sensu Verte. . .; TAS.  
DR GO; GO:0006874; P:calcium ion homeostasis; TAS.  
DR GO; GO:0006928; P:cell motility; TAS.  
DR GO; GO:0007267; P:cell-cell signaling; TAS.  
DR GO; GO:0006935; P:chemotaxis; TAS.  
DR GO; GO:0007010; P:cytoskeleton organization and biogenesis; TAS.  
DR GO; GO:0006887; P:exocytosis; TAS.  
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; TAS.  
DR GO; GO:0006954; P:inflammatory response; TAS.  
DR GO; GO:0045069; P:regulation of viral genome replication; TAS.  
DR GO; GO:0007165; P:signal transduction; TAS.  
DR InterPro; IPR000827; CC\_chemokine\_sm1.  
DR InterPro; IPR001811; Chemokine\_IL8.  
DR Pfam; PF00048; IL8; 1.  
DR PROSITE; PS00472; SMALL\_CYTOKINES\_CC; 1.

KW 3D-structure; Chemotaxis; Cytokine; Direct protein sequencing;  
KW Inflammatory response; Signal.  
FT SIGNAL 1 23  
FT CHAIN 24 92 Small inducible cytokine A3.  
FT CHAIN 27 92 MIP-1-alpha(4-69).  
FT DISULFID 33 57 By similarity.  
FT DISULFID 34 73 By similarity.  
FT MUTAGEN 49 49 D->A: Reduces self-association; in BB-  
FT 10010: Improved pharmaceutical  
FT 10010: Improves self-association.  
FT MUTAGEN 89 89 E->A: Reduces self-association.  
FT TURN 44 46  
FT STRAND 49 51  
FT TURN 55 58  
FT STRAND 63 65  
FT TURN 67 68  
FT TURN 76 77  
FT HELIX 79 84  
FT TURN 85 88  
SQ SEQUENCE 92 AA; 10085 MW; 517865D5D6776CA8 CRC64;  
Query Match 46.8%; Score 236; DB 1; Length 92;  
Best Local Similarity 48.4%; Pred. No. 4.5e-19;  
Matches 44; Conservative 22; Mismatches 23; Indels 2; Gaps 2;  
QY 1 MKISVAIPFELLITIALGTCTESSRGYPHPSECCFTYTYKIPQRIMDYETNSQCS 60  
DB 1 MOVSTAALA-VLCTWALCNQP-SASLAADTTFACFSYTSRQIFQNFADIFETSSQCS 58  
QY 61 KFGIVFTIKRGHSVCTNPSDKWQDYIKDMK 91  
DB 59 KFGVFLTKRSRQVCADPSEWVQKVSLE 89  
RESULT 8  
SY04 CHICK STANDARD; PRT; 90 AA.  
AC Q04826; Q910C9;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 28-FEB-2004 (Rel. 41, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Small inducible cytokine A4 homolog precursor (Macrophage inflammatory  
DE protein 1-beta homolog).  
GN Name=CCL4; Synonyms=SCY44;  
OS Gallus gallus (Chicken)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.  
OX NCBI\_TaxID=9031;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Bone marrow;  
RX MEDLINE=95369710; PubMed=7642115; DOI=10.1016/0378-1119(95)00210-W;  
RA Petrenko O., Ischenko I., Enrietto P.J.;  
RT "Isolation of a cDNA encoding a novel chicken chemokine homologous to  
RT mammalian macrophage inflammatory protein-1 beta.";  
RL Gene 160:305-306(1995).  
[2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20049023; PubMed=10582310;  
RA Hughes S., Bumstead N.;  
RT "Mapping of the gene encoding a chicken homologue of the mammalian  
RT chemokine SCY44.";  
RL Anim. Genet. 30:404-404(1999).  
[3]  
RP SEQUENCE OF 14-90 FROM N.A.  
RA Petrenko O., Enrietto P.J.;  
RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: Monokine with inflammatory and chemokinetic properties  
CC (By similarity).  
CC -!- SUBUNIT: Homodimer (By similarity).  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: Belongs to the interleukin beta (chemokine CC) family.



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DR EMBL; AF128219; AAF22560.1; -.
DR PIR; C30552; C30552.
DR HSSP; P13236; IHUM.
DR MGD; MGI:98261; Cc14.
DR InterPro; IPR000827; CC_chemkine_sml.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR SMART; SM00199; SCY; 1.
DR PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
KW Chemotaxis; Cytokine; Inflammatory response; Signal.
FT SIGNAL 1 23
FT CHAIN 24 92 Small inducible cytokine A4.
FT DISULFID 34 58 By similarity.
FT DISULFID 35 74 By similarity.
SQ SEQUENCE 92 AA; 10168 MW; 8853FD58FDE61BAC CRC64;

Query Match 46.5%; Score 234.5; DB 1; Length 92;
Best Local Similarity 45.2%; Pred. No. 6.7e-19;
Matches 42; Conservative 20; Mismatches 30; Indels 1; Gaps 1;

QY 1 MKISVAIPFFLLITLALGKTGTESSRGPYHPSECCFTYTYKIPRQIMDYETNSQCS 60
DB 1 MKLCVSFSLLLVA-AFCAPGSPMGSDPPTCCFSYTSRQLHRSFVMDYETSLCS 59

QY 61 KPGIVFITKRGHSVCTNPSPDKVQDYIKDMKEN 93
DB 60 KPAVVFITKRGICANPSPWPWTEYMSDLELN 92

RESULT 11
SY04_RABIT
ID SY04_RABIT STANDARD; PRT; 92 AA.
AC P46632;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Small inducible cytokine A4 precursor (CC14) (Macrophage inflammatory
DE protein 1-beta) (MIP-1-beta) (Immune activation protein 2) (ACT-2).
GN Names=CC14; Synonyms=SCYA4;
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=New Zealand white;
RX MEDLINE=94198229; PubMed=8148323;
RA Mori S., Goto K., Goto F., Mutakami K., Ohkawara S., Yoshinaga M.;
RT "Dynamic changes in mRNA expression of neutrophils during the course
RT of acute inflammation in rabbits.";
RL Int. Immunol. 6:149-156(1994).
CC -1- FUNCTION: Monokine with inflammatory and chemokinetic properties
CC (By similarity).
CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the intercrine beta (chemokine CC) family.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; D17402; BAA04226.1; -.
DR PIR; I46730; I46730.
DR HSSP; P13236; IHUM.
DR InterPro; IPR000827; CC_chemkine_sml.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR SMART; SM00199; SCY; 1.
DR PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.

```

```

KW Chemotaxis; Cytokine; Inflammatory response; Signal.
FT SIGNAL 1 23 By similarity.
FT CHAIN 24 92 Small inducible cytokine A4.
FT DISULFID 34 58 By similarity.
FT DISULFID 35 74 By similarity.
SQ SEQUENCE 92 AA; 10066 MW; ECBA8818D42A735C CRC64;

Query Match 45.7%; Score 230.5; DB 1; Length 92;
Best Local Similarity 45.2%; Pred. No. 1.9e-18;
Matches 42; Conservative 18; Mismatches 32; Indels 1; Gaps 1;

QY 1 MKISVAIPFFLLITLALGKTGTESSRGPYHPSECCFTYTYKIPRQIMDYETNSQCS 60
DB 1 MKLGVTVLSVALLVA-ALCPPALSAPMGSDPPTACCFSTLRKLPFRHFDYFETSLCS 59

QY 61 KPGIVFITKRGHSVCTNPSPDKVQDYIKDMKEN 93
DB 60 QPAVVFQTKKRGQVCANPSESQVQYVDLELN 92

RESULT 12
SY04_RAT
ID SY04_RAT STANDARD; PRT; 92 AA.
AC P50230;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Small inducible cytokine A4 precursor (CC14) (Macrophage inflammatory
DE protein 1-beta) (MIP-1-beta).
GN Name=CC14; Synonyms=Mip1b, Scya4;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Long Evans; TISSUE=Lung;
RA Jones M.L., Shanley T.P., Schmal H., Friedl H.P., Ward P.A.;
RL Submitted (FEB-1994) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Monokine with inflammatory and chemokinetic properties.
CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the intercrine beta (chemokine CC) family.
CC
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CC
CC EMBL; U06434; AAA96497.1; -.
DR HSSP; P13236; IHUM.
DR InterPro; IPR000827; CC_chemkine_sml.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR SMART; SM00199; SCY; 1.
DR PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
KW Chemotaxis; Cytokine; Inflammatory response; Signal.
FT SIGNAL 1 23 By similarity.
FT CHAIN 24 92 Small inducible cytokine A4.
FT DISULFID 34 58 By similarity.
FT DISULFID 35 74 By similarity.
SQ SEQUENCE 92 AA; 10234 MW; 60B451EEBC7103D CRC64;

Query Match 45.5%; Score 229.5; DB 1; Length 92;
Best Local Similarity 44.1%; Pred. No. 2.5e-18;
Matches 41; Conservative 20; Mismatches 31; Indels 1; Gaps 1;

QY 1 MKISVAIPFFLLITLALGKTGTESSRGPYHPSECCFTYTYKIPRQIMDYETNSQCS 60
DB 1 MKLCVSFSLLLVA-AFCDSVLSAPIGSDPPTCCFSYTSRKIHNFVMDYETSLCS 59

```

[illegible]

[Contains: MIP-1-beta(3-69)].

DE Name=CCl4; Synonyms=LAG1, MIP1B, SCV44;

GN Homo sapiens (Human).

OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=89071764; PubMed=2462251;

RA Lipes M.A., Napolitano M., Jeang K.-T., Chang N.T., Leonard W.J.;

RT "Mitogenic activation of human T cells induces two closely related

RT genes which share structural similarities with a new family of

RT secreted factors.";

RL J. Immunol. 142:1582-1590(1989).

RN [3]

RP SEQUENCE FROM N.A.

RX MEDLINE=89093958; PubMed=2521353;

RA Brown K.D., Zurawski S.M., Mosmann T.R., Zurawski G.;

RT "A family of small inducible proteins secreted by leukocytes are

RT members of a new superfamily that includes leukocyte and fibroblast-

RT derived inflammatory agents, growth factors, and indicators of various

RT activation processes.";

RL J. Immunol. 142:679-687(1989).

RN [4]

RP SEQUENCE FROM N.A.

RX MEDLINE=91061800; PubMed=2247088; DOI=10.1016/0161-5890(90)90097-J;

RA Baixeras E., Roman-Roman S., Jitsukawa S., Genevee C., Mechiche S.,

RT Viégas-Pequignot E., Hercend T., Triebel F.;

RT "Cloning and expression of a lymphocyte activation gene (LAG-1).";

RL Mol. Immunol. 27:1091-1102(1990).

RN [5]

RP SEQUENCE FROM N.A.

RC TISSUE=T-cell;

RX MEDLINE=89325421; PubMed=2568930;

RA Chang H.C., Reinherz E.L.;

RT "Isolation and characterization of a cDNA encoding a putative cytokine

RT which is induced by stimulation via the CD2 structure on human T

RT lymphocytes.";

RL Eur. J. Immunol. 19:1045-1051(1989).

RN [6]

RP SEQUENCE FROM N.A.

RX MEDLINE=91373378; PubMed=1894635;

RA Napolitano M., Modi W.S., Cevalero S.J., Gnarr J.R., Seuanez H.N.,

RA Leonard W.J.;

RT "The gene encoding the Act-2 cytokine. Genomic structure, HTLV-I/Tax

RT responsiveness of 5' upstream sequences, and chromosomal

RT localization.";

RL J. Biol. Chem. 266:17531-17536(1991).

RN [7]

RP SEQUENCE FROM N.A.

RA Birren B., Fasman K., McKernan K., Nusbaum C., Richardson P.,

RA Lander E.;

RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.

RN [8]

RP SEQUENCE OF 6-92 FROM N.A.

RX MEDLINE=90038522; PubMed=2809212;

RA Miller M.D., Hata S., Waal Malefyt R., Krangel M.S.;

RT "A novel polypeptide secreted by activated human T lymphocytes.";

RL J. Immunol. 143:2907-2916(1989).

RN [9]

RP RECEPTOR INTERACTION.

RX MEDLINE=98180363; PubMed=9521068;

RA DOI=10.1002/(SICI)1521-4141(199802)28:02<582::AID-IMMU582>3.3.CO;2-1;

RA Bernardini G., Hedrick J., Sozzani S., Luini W., Spinetti G.,

RA Weiss M., Menon S., Zlotnik A., Mantovani A., Santoni A.,

RA Napolitano M.;

RT "Identification of the CC chemokines TARC and macrophage inflammatory

RT protein-1 beta as novel functional ligands for the CCR8 receptor.";

RL Eur. J. Immunol. 28:582-588(1998).

RN [10]

RP FUNCTION.

RX MEDLINE=96106406; PubMed=8525373;

RA Cocchi F., DeVico A.L., Garzino-Demo A., Arya S.K., Gallo R.C.,

RA Lusso P.;

RT "Identification of RANTES, MIP-1 alpha, and MIP-1 beta as the major

RT HIV-suppressive factors produced by CD8+ T cells.";

RL Science 270:1811-1815(1995).

RN [11]

RP IDENTIFICATION OF MIP-1-BETA(3-69) BY MASS SPECTROMETRY, FUNCTION, AND

RP SUBUNIT.

RX PubMed=12070155; DOI=10.1074/jbc.M203077200;

RA Guan E., Wang J., Roderiquez G., Norcross M.A.;

RT "Natural truncation of the chemokine MIP-1beta /CCL4 affects receptor

RT specificity but not anti-HIV-1 activity.";

RL J. Biol. Chem. 277:32348-32352(2002).

RN [12]

RP REVIEW.

RX PubMed=12401480; DOI=10.1016/S1359-6101(02)00045-X;

RA Menten P., Whyts A., Van Damme J.;

RT "Macrophage inflammatory protein-1.";

RL Cytokine Growth Factor Rev. 13:455-481(2002).

RN [13]

RP STRUCTURE BY NMR.

RX MEDLINE=94182137; PubMed=8134838;

RA Lodi P.J., Garrett D.S., Kuscewski J., Tsang M.L.S., Weatherbee J.A.,

RA Leonard W.J., Gronenborn A.M., Clore G.M.;

RT "High-resolution solution structure of the beta chemokine hMIP-1 beta

RT by multidimensional NMR.";

RL Science 263:1762-1767(1994).

CC -!- FUNCTION: Monokine with inflammatory and chemokinetic properties.

CC Binds to CCR5 and to CCR8. One of the major HIV-suppressive

CC factors produced by CD8+ T cells. Recombinant MIP-1-beta induces a

CC dose-dependent inhibition of different strains of HIV-1, HIV-2,

CC and simian immunodeficiency virus (SIV). The processed form MIP-1-

CC beta(3-69) retains the abilities to induce down-modulation of

CC surface expression of the chemokine receptor CCR5 and to inhibit

CC the CCR5-mediated entry of HIV-1 in T cells. MIP-1-beta(3-69) is

CC also a ligand for CCR1 and CCR2 isoform B.

CC -!- SUBUNIT: Homodimer and heterodimer of MIP-1-alpha(4-69) and MIP-1-

CC beta(3-69).

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- INDUCTION: By mitogens.

CC -!- PTM: N-terminal processed form MIP-1-beta(3-69) is produced by

CC proteolytic cleavage after secretion from peripheral blood

CC lymphocytes.

CC -!- SIMILARITY: Belongs to the intercrine beta (chemokine CC) family.

CC -----

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CC -----

DR EMBL; M23502; AAA36656.1; -.

DR EMBL; M25316; AAA57256.1; -.

DR EMBL; J04130; AAA51576.1; -.

DR EMBL; X51683; CAA37723.1; -.

DR EMBL; X53682; CAA37722.2; ALT\_SEQ.

DR EMBL; X16166; CAA34231.1; -.

DR EMBL; M69203; AAB00790.1; -.

DR EMBL; M69201; AAB00790.1; JOINED.

DR EMBL; M69202; AAB00790.1; JOINED.

DR EMBL; AC003976; -; NOT ANNOTATED\_CDS.

DR EMBL; M57503; AAA36752.1; -.

DR PIR; JH0319; A31767.

DR PDB; 1HUN; NMR; A/B=24-92.

DR PDB; 1HUN; NMR; A/B=24-92.



PDB: 1JEA; NMR: A=24-92.  
DR GEM; HGNC:10630; CCL4.  
DR MIN; 182284; -.  
DR GO: GO:0005615; C:extracellular space; TAS.  
DR GO: GO:0008009; F:chemokine activity; TAS.  
DR GO: GO:0047116; P:receptor signaling protein tyrosine kinase . . .; TAS.  
DR GO: GO:0007155; P:cell adhesion; TAS.  
DR GO: GO:0008131; P:cell growth and/or maintenance; TAS.  
DR GO: GO:0006928; P:cell motility; TAS.  
DR GO: GO:0007163; P:establishment and/or maintenance of cell po. . .; TAS.  
DR GO: GO:0006955; P:immune response; TAS.  
DR GO: GO:0009544; P:inflammatory response; TAS.  
DR GO: GO:0009615; P:response to virus; TAS.  
DR GO: GO:0019079; P:signal transduction; TAS.  
DR InterPro: IPR000827; CC chemokine sml.  
DR InterPro: IPR001811; Chemokine\_IL8.  
DR Pfam: PF00048; IL8; 1.  
DR SMART: SM00199; SCY; 1.  
DR PROSITE: PS00472; SMALL CYTOKINES CC; 1.  
KW 3D-structure; Chemotaxis; Cytokine; Inflammatory response; Signal.  
FT SIGNAL 1 23 Small inducible cytokine A4.  
FT CHAIN 24 92 MIP-1-beta(3-69).  
FT CHAIN 26 92 By similarity.  
FT DISULFID 34 58 By similarity.  
FT CONFLICT 35 74 T -> C (in Ref. 7).  
FT CONFLICT 6 6 A -> S (in Ref. 6).  
FT CONFLICT 15 15 P -> L (in Ref. 2).  
FT CONFLICT 20 20 ARKLPK -> REAS (in Ref. 3).  
FT CONFLICT 40 45 S -> I (in Ref. 8).  
FT CONFLICT 56 56 S -> G (in Ref. 6).  
FT CONFLICT 70 70 S -> T (in Ref. 7 and 8).  
FT CONFLICT 80 80  
FT STRAND 29 29  
FT STRAND 33 33  
FT HELIX 45 47  
FT STRAND 50 53  
FT STRAND 63 66  
FT STRAND 72 75  
FT TURN 77 78  
FT HELIX 80 92  
SQ SEQUENCE 92 AA; 10212 MW; F2EA7CF341B0E258 CRC64;  
Query Match 44.5%; Score 224.5; DB 1; Length 92;  
Best Local Similarity 43.0%; Pred. No. 9.3e-18;  
Matches 40; Conservative 20; Mismatches 32; Indels 1; Gaps 1;  
Qy 1 MKISVAIPFLLITIALGTKESSSRGPHYHPCCTTYTKIPRQIMDYETNSQCS 60  
Db 1 MKLCVTLSLLMLVA-AFCSPALSPMGSDPTACCFSTARKLPFRNFVVDYETSLCS 59  
Qy 61 KPGIVFTKRGHVCVTNPSPDKVQDYIKDMKEN 93  
Db 60 QPAVVFTKRGKQVCADPSESQVQYVDLELN 92  
RESULT 17  
Q6NSB0 PRELIMINARY; PRT; 92 AA.  
AC Q6NSB0  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Chemokine (C-C motif) ligand 4-like 1.  
GN Name=CCL4L1;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Pooled;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP TISSUE=Pooled;  
RA Strausberg R.;  
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC070310; AAH70310.1; -.  
DR HSSP; P10147; 1B50.  
DR GO: GO:0005576; C:extracellular; IEA.  
DR GO: GO:0008009; F:chemokine activity; IEA.  
DR GO: GO:0006955; P:immune response; IEA.  
DR InterPro: IPR000827; CC chemokine sml.  
DR InterPro: IPR001811; Chemokine\_IL8.  
DR Pfam: PF00048; IL8; 1.  
DR SMART: SM00199; SCY; 1.  
DR PROSITE: PS00472; SMALL CYTOKINES CC; 1.  
SQ SEQUENCE 92 AA; 10147 MW; 6A567D8926CDE89F CRC64;  
Query Match 44.3%; Score 223.5; DB 2; Length 92;  
Best Local Similarity 43.0%; Pred. No. 1.2e-17;  
Matches 40; Conservative 20; Mismatches 32; Indels 1; Gaps 1;  
Qy 1 MKISVAIPFLLITIALGTKESSSRGPHYHPCCTTYTKIPRQIMDYETNSQCS 60  
Db 1 MKLCVTLSLLMLVA-AFCSPALSPMGSDPTACCFSTARKLPFRNFVVDYETSLCS 59  
Qy 61 KPGIVFTKRGHVCVTNPSPDKVQDYIKDMKEN 93  
Db 60 QPAVVFTKRGKQVCADPSESQVQYVDLELN 92  
RESULT 18  
SY03 MOUSE  
ID SY03 MOUSE STANDARD; PRT; 92 AA.  
AC P10855; P14096;  
DT 01-JUL-1989 (Rel. 11, Created)  
DT 01-APR-1990 (Rel. 14, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Small inducible cytokine A3 precursor (CCL3) (Macrophage inflammatory  
DE protein 1-alpha) (MIP-1-alpha) (TY-5) (SIS-alpha) (Heparin-binding  
DE chemotaxis protein) (L2G25B).  
GN Name=Ccl3; Synonyms=Mipla, Scya3;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX Davatelis G., Tekamp-Olson P., Wolpe S.D., Hermesen K., Luedke C.,  
RA Gallegos C., Coit D., Merryweather J., Cerami A.;  
RT "Cloning and characterization of a cDNA for murine macrophage  
RT inflammatory protein (MIP), a novel monokine with inflammatory and



RP SEQUENCE OF 24-57.  
RC STRAIN=Wistar;  
RX MEDLINE=96183056; PubMed=8607872; DOI=10.1006/bbrc.1996.0511;  
RA Nakagawa H., Shota S., Takano K., Shibata F., Kato H.;  
RT "Cytokine-induced neutrophil chemoattractant (CINC)-2 alpha, a novel  
RT member of rat GRO/CINC, is a predominant chemokine produced by  
RT lipopolysaccharide-stimulated rat macrophages in culture.";  
RL Biochem. Biophys. Res. Commun. 220:945-948(1996).  
CC -!- FUNCTION: Monokine with inflammatory and chemokinetic properties.  
CC Has chemotactic activity for monocytes, neutrophils, eosinophils,  
CC basophils, and lymphocytes. Required for lung TNF-alpha  
CC production, neutrophil recruitment and subsequent lung injury and  
CC may function as an autocrine mediator for the macrophage  
CC production of TNF-alpha which in turn up-regulates vascular  
CC adhesion molecules required for neutrophil influx. This protein  
CC binds heparin.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- INDUCTION: By lipopolysaccharide (LPS).  
CC -!- SIMILARITY: Belongs to the interleukin beta (chemokine CC) family.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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CC -----  
DR EMBL; U22414; AAA80608.1; -;  
DR EMBL; U06435; AAA96498.1; -;  
DR PIR; I52322; I52322.  
DR HSP; P10147; I850.  
DR RGD; 3647; Cc13.  
DR InterPro; IPR000827; CC chemokine sm1.  
DR InterPro; IPR001811; Chemokine\_IL8.  
DR Pfam; PF00048; IL8; 1.  
DR SMART; SM00199; SCV; 1.  
DR PROSITE; PS00472; SMALL\_CYTOKINES\_CC; 1.  
KW Chemotaxis; Cytokine; Direct protein sequencing; Heparin-binding;  
KW Inflammatory response; Signal.  
FT SIGNAL 1 23  
FT CHAIN 24 92 Small inducible cytokine A3.  
FT DISULFID 34 57 By similarity.  
FT DISULFID 35 73 By similarity.  
FT CONFLICT 6 6 A -> T (in Ref. 2).  
FT CONFLICT 57 57 C -> W (in Ref. 2 and 3).  
SQ SEQUENCE 92 AA; 10335 MW; 14B861C647F9A2EB CRC64;  
Query Match 44.2%; Score 223; DB 1; Length 92;  
Best Local Similarity 45.2%; Pred. No. 1.4e-17;  
Matches 42; Conservative 22; Mismatches 27; Indels 2; Gaps 2;  
QY 1 MKISVAAIPFLLITIALGKTSSRGYPHSPCCFTYTYKIPRQIMDYETNSQCS 60  
DB 1 MKYSTAALA-VLLCTMALNWEVFSAPYGADPTACCFSGYGR-QIPRKFADYFETSSLS 58  
QY 61 KPGIVITKRGHSVCTNPSDKWQDYIKDKMEN 93  
DB 59 QPGVIFLTKRNRQICADPKETWQYETILELN 91  
RESULT 20  
Q91ZLO PRELIMINARY; PRT; 92 AA.  
AC Q91ZLO;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Macrophage inflammatory protein 1 beta.  
GN Name=MIP-1beta;  
OS Sigmodon hispidus (Hispid cotton rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;

OC Sigmodon.  
OX NCBI\_TaxID=42415;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22079879; PubMed=12085325;  
RA Blanco J.C., Richardson J.Y., Darnell M.E., Rowzee A., Pletneva L.,  
RA Porter D.D., Prince G.A.;  
RT "Cytokine and chemokine gene expression after primary and secondary  
RT respiratory syncytial virus infection in cotton rats.";  
RL J. Infect. Dis. 185:1780-1785(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX PubMed=1498081; DOI=10.1089/107999004772719873;  
RA Blanco J.C., Pletneva L., Boukhalova M., Richardson J.Y.,  
RA Harris K.A., Prince G.A.;  
RT "The cotton rat: an underutilized animal model for human infectious  
RT diseases can now be exploited using specific reagents to cytokines,  
RT chemokines, and interferons.";  
RL J. Interferon Cytokine Res. 24:21-28(2004).  
DR EMBL; AF421392; AAL16933.1; -;  
DR HSP; P12336; IHUM.  
DR GO; GO:0005576; C:extracellular; IEA.  
DR GO; GO:0008009; F:chemokine activity; IEA.  
DR GO; GO:0006955; P:immune response; IEA.  
DR Pfam; PF00048; IL8; 1.  
DR SMART; SM00199; SCV; 1.  
DR PROSITE; PS00472; SMALL\_CYTOKINES\_CC; 1.  
SQ SEQUENCE 92 AA; 10195 MW; A34FDE21E6FA9C2B CRC64;  
Query Match 44.1%; Score 222.5; DB 2; Length 92;  
Best Local Similarity 41.9%; Pred. No. 1.6e-17;  
Matches 39; Conservative 20; Mismatches 33; Indels 1; Gaps 1;  
QY 1 MKISVAAIPFLLITIALGKTSSRGYPHSPCCFTYTYKIPRQIMDYETNSQCS 60  
DB 1 MKLCLSTLALLLLAEFCAPVT-SAPRGSDPPISCCFSYASRKLPRNFVDYVETSSLS 59  
QY 61 KPGIVITKRGHSVCTNPSDKWQDYIKDKMEN 93  
DB 60 KPAVVELTRKGEVCADPSQPVWYVNDLELN 92  
RESULT 21  
Q68A92 PRELIMINARY; PRT; 92 AA.  
AC Q68A92;  
DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
DE CC chemokine ligand 3.  
GN Name=CCL3;  
OS Canis familiaris (Dog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
OX NCBI\_TaxID=9615;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Teukui T., Sakaguchi M., Maeda S., Koyanagi M., Masuda K., Ohno K.,  
RA Tsujimoto H., Iwabuchi S.;  
RT "Expression analysis of gene in canine atopic dermatitis.";  
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB164618; BAD42447.1; -;  
DR InterPro; IPR001811; Chemokine\_IL8.  
DR Pfam; PF00048; IL8; 1.  
DR SMART; SM00199; SCV; 1.  
SQ SEQUENCE 92 AA; 10029 MW; 9D44596B37FD6910 CRC64;  
Query Match 43.7%; Score 220; DB 2; Length 92;  
Best Local Similarity 47.3%; Pred. No. 3e-17;  
Matches 43; Conservative 20; Mismatches 26; Indels 2; Gaps 2;  
QY 1 MKISVAAIPFLLITIALGKTSSRGYPHSPCCFTYTYKIPRQIMDYETNSQCS 60  
DB 1 MKISVAAIPFLLITIALGKTSSRGYPHSPCCFTYTYKIPRQIMDYETNSQCS 60

Db	1	MKVPGAALA-VLLCTMSLCSQV-FSPFGADTPIACCFSVYVKQIPRKFIIVDCPETSSQCS	58
Qy	61	KPGIVFTRKGHSVCTNPNPSDKWQDYIKMK	91
Db	59	KPGIIFETRKGRQACANPSEAWQOEVYADLK	89
RESULT 22			
Q80XG5	Q80XG5	PRELIMINARY;	PRT; 85 AA.
AC	Q80XG5;		
DT	01-JUN-2003 (TREMBLrel. 24, Created)		
DT	01-JUN-2003 (TREMBLrel. 24, Last sequence update)		
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)		
DE	CC chemokine ligand 4 (Fragment).		
GN	Name=Ccl4;		
OS	Peromyscus maniculatus (Deer mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;		
OC	Peromyscus.		
OX	NCBI_TaxID=10042;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Schountz T., Buniger A., Davenport B., Hegg T.;		
RT	"Cloning of deer mouse IL-2, IL-12 p35, IL-21, GM-CSF, CCL3 and CCL4		
RT	cDNAs."		
RL	Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AY247758; AAP04417.1; -.		
DR	HSSP; P13236; IHUM.		
DR	GO; GO:0005576; C:extracellular; IEA.		
DR	GO; GO:0008009; F:chemokine activity; IEA.		
DR	GO; GO:0006955; P:immune response; IEA.		
DR	InterPro; IPR000827; CC-chemokine sml.		
DR	InterPro; IPR001811; Chemokine_IL8.		
DR	Pfam; PF00048; IL8; 1.		
DR	SMART; SM00199; SCY; 1.		
DR	PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.		
FT	NON_TER	85	
SQ	SEQUENCE	85 AA; 9345 MW; B87216B9B41F34C	CRC64;
Query Match 43.2%; Score 217.5; DB 2; Length 85;			
Best Local Similarity 45.3%; Pred. No. 5.4e-17;			
Matches 39; Conservative 17; Mismatches 29; Indels 1; Gaps 1;			
Qy	1	MKLSVAIPFLITLALGCTKTSSRGPHVSECCFTYTYKIPRQIMDYVETNSQCS	60
Db	1	MKLCSALSFLVVA-AFWAPALSAPMGDPPTSCCFSTYARKLPNFTVDYVETSSLCS	59
Qy	61	KPGIVFTRKGHSVCTNPNPSDKWQDY	86
Db	60	KPAVFLTRKGKQVCADPSLPWNEY	85
RESULT 23			
Q14745	Q14745	PRELIMINARY;	PRT; 80 AA.
AC	Q14745;		
DT	01-NOV-1996 (TREMBLrel. 01, Created)		
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)		
DT	01-JUN-2003 (TREMBLrel. 24, Last annotation update)		
DE	LD78 alpha beta precursor (Fragment).		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Brain;		
RA	Ishizuka K., Igata-yi R., Naruse K., Nakashima H., Ohuchi K.,		
RA	Katsuragi S., Kin Y., Ohmoto Y., Nomiya H., Iio M., Miura R.,		
RA	Miyakawa T.;		
RL	Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; D63785; BAA09855.1; -.		
DR	HSSP; P10147; IB50.		
DR	GO; GO:0005576; C:extracellular; IEA.		
DR	GO; GO:0008009; F:chemokine activity; IEA.		
DR	GO; GO:0006955; P:immune response; IEA.		
DR	InterPro; IPR000827; CC-chemokine sml.		
DR	InterPro; IPR001811; Chemokine_IL8.		
DR	Pfam; PF00048; IL8; 1.		
DR	SMART; SM00199; SCY; 1.		
DR	PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.		
FT	NON_TER	1	
SQ	SEQUENCE	56 AA; 6442 MW; EB12A0E0D41D6F68	CRC64;
Query Match 41.5%; Score 209; DB 2; Length 56;			
Best Local Similarity 57.1%; Pred. No. 3.3e-16;			
Matches 32; Conservative 14; Mismatches 10; Indels 0; Gaps 0;			
Qy	32	PSECCFTYTYKIPRQIMDYVETNSQCSKPGIVFTRKGHSVCTNPNPSDKWQDYI	87
Db	1	PTACCFSTYTRQIPQNFADYFETSSQCSKPGIVFLTKRSRQVCADPSEEWQKYV	56

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RESULT 25
Q918E0 PRELIMINARY; PRT; 89 AA.
ID AC Q918E0;
AD Q918E0;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Chemokine K203 precursor.
GN Name=K203;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20170941; PubMed=10704244; DOI=10.1006/cyto.1999.0543;
RA Sick C., Schneider K., Staeheli P., Weining K.C.;
RT "Novel chicken CXc and CC chemokines.";
RL EMBL; Y18692; CAB70956.1; -.
DR HSSP; Q16663; 2HCC.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008009; F:chemokine activity; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR SMART; SM00199; SCY; 1.
KW Signal.
FT SIGNAL 1 21 Potential.
FT CHAIN 22 89 Chemokine K203.
SQ SEQUENCE 89 AA; 9896 MW; 6FA2EA7A4950CA75 CRC64;

Query Match 41.5%; Score 209; DB 2; Length 89;
Best Local Similarity 43.0%; Pred. No. 5.3e-16;
Matches 40; Conservative 18; Mismatches 31; Indels 4; Gaps 2;

Qy 1 MKISVAIPPELLITIALGTKESSRGYPHPSCCFYTYTKIPRQIMDYETNSQCS 60
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 1 MKLSAVVL---ALLIASFCSSASSAPVGPDPVT-CCTTYTHKIPRNLIQRHYSTSTSCS 56

Qy 61 KPGIVFTKRGHSVCTNPSPDWQDYIKDMKEN 93
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 57 KPAIFITTKEREVCANPDPWQVQLQSVKRD 89

RESULT 26
SY18_HUMAN STANDARD; PRT; 89 AA.
ID SY18_HUMAN
AC P55774;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUN-2004 (Rel. 44, Last annotation update)
DE Small inducible cytokine A18 precursor (CC118) (Macrophage
DE inflammatory protein 4) (MIP-4) (Pulmonary and activation-regulated
DE chemokine) (CC chemokine PARC) (Alternative macrophage activation-
DE associated CC chemokine 1) (AMAC-1) (Dendritic cell chemokine 1) (DC-
DE CK1).
GN Name=CC118; Synonyms=AMAC1, DCC1, MIP4, PARC, SCYA18;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Li H., Ruben S.;
RT "Macrophage inflammatory protein-3 and -4.";
RL Patent number US5504003, 02-APR-1996.
RN [2]
RP SEQUENCE FROM N.A.; AND PARTIAL SEQUENCE.
RC TISSUE=Aorta, and Lung;
RX MEDLINE=97376836; PubMed=9233607;

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RA Hieshima K., Imai T., Baba M., Shoudai K., Ishizuka K., Nakagawa T.,
RA Tsuruta J., Takeya M., Sakaki Y., Takatsuki K., Miura R.,
RA Odenakker G., van Damme J., Yoshie O., Nomiya H.;
RT "A novel human CC chemokine PARC that is most homologous to
RT macrophage-inflammatory protein-1 alpha/LD78 alpha and chemotactic for
RT T lymphocytes, but not for monocytes.";
RL J. Immunol. 159:1140-1149(1997).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=98230488; PubMed=9570561;
RA Kodelja V., Mueller C., Politz O., Haki N., Orfanos C.E., Goerd S.;
RT "Alternative macrophage activation-associated CC-chemokine-1, a novel
RT structural homologue of macrophage inflammatory protein-1 alpha with a
RT Th2-associated expression pattern.";
RL J. Immunol. 160:1411-1418(1998).
RN [4]
RP DISCUSSION OF SEQUENCE.
RX MEDLINE=97275308; PubMed=9129202;
RA Wells T.N.C., Peitsch M.C.;
RT "The chemokine information source: identification and characterization
RT of novel chemokines using the WorldWideWeb and expressed sequence tag
RT databases.";
RL J. Leukoc. Biol. 61:545-550(1997).
RN [5]
RP SEQUENCE FROM N.A., AND SEQUENCE OF N-TERMINUS.
RX TISSUE=Dendritic cell;
RL MEDLINE=97336102; PubMed=912897; DOI=10.1038/42716;
RA Adema G.J., Hartgers F., Verstraten R., de Vries E., Marland G.,
RA Menon S., Foster J., Xu Y., Nooyen P., McClanahan T., Bacon K.B.,
RA Figdor C.G.;
RT "A dendritic-cell-derived C-C chemokine that preferentially attracts
RT naive T cells.";
RL Nature 387:713-717(1997).
RN [6]
RP SEQUENCE FROM N.A.
RX MEDLINE=99168908; PubMed=10049593; DOI=10.1006/geno.1998.5670;
RA Tasaki Y., Fukuda S., Iio M., Miura R., Inai T., Sugano S., Yoshie O.,
RA Hughes A.L., Nomiya H.;
RT "Chemokine PARC gene (SCYA18) generated by fusion of two MIP-
RT 1alpha/LD78alpha-like genes.";
RL Genomics 55:353-357(1999).
RN [7]
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
RX MEDLINE=99189237; PubMed=10087196; DOI=10.1006/geno.1998.5635;
RA Guan P., Burghes A.H.M., Cunningham A., Lira P., Briessette W.H.,
RA Neote K., McCall S.R.;
RT "Genomic organization and biological characterization of the novel
RT human CC chemokine DC-CK-1/PARC/MIP-4/SCYA18.";
RL Genomics 56:296-302(1999).
RN [8]
RP SEQUENCE FROM N.A.
RA Politz O., Kodelja V., Guillot P., Orfanos C.E., Goerd S.;
RT "The genomic locus for the AMAC-1 gene contains possible pseudo-exons
RT within the first intron sequence.";
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Chemotactic factor that attracts lymphocytes but not
CC monocytes or granulocytes. May be involved in B cell migration
CC into B cell follicles in lymph nodes. Attracts naive T lymphocytes
CC toward dendritic cells and activated macrophages in lymph nodes.
CC has chemotactic activity for naive T cells, CD4+ and CD8+ T cells
CC and thus may play a role in both humoral and cell-mediated
CC immunity responses.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed at high levels in lung, lymph nodes,
CC placenta, bone marrow, dendritic cells present in germinal centers
CC and T-cell areas of secondary lymphoid organs and macrophages
CC derived from peripheral blood monocytes. Not expressed by
CC peripheral blood monocytes and a monocyte-to-macrophage
CC differentiation is a prerequisite for expression.
CC -1- INDUCTION: Specifically induced in macrophages by IL-4, IL-13, and
CC IL-10. Expression is inhibited by IFN-gamma while glucocorticoids
CC exert a slightly positive synergistic effect in combination with
CC IL-4. Strongly induced in several human cell lines, including

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DR EMBL; U58913; AAD10846.1; -.
DR EMBL; U67128; AAD00161.1; -.
DR EMBL; AF088219; AAC63326.1; -.
DR EMBL; AF088219; AAC63327.1; -.
DR PDB; 1C91; NMR; A=44-120.
DR Genew; HGNC:10622; CCL23.
DR MIM; 602494; -.
DR GO; GO:0008009; F:chemokine activity; TAS.
DR GO; GO:0006874; P:calcium ion homeostasis; TAS.
DR GO; GO:0007267; P:cell-cell signaling; TAS.
DR GO; GO:0006935; P:chemotaxis; TAS.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; TAS.
DR GO; GO:0006955; P:immune response; TAS.
DR GO; GO:0006954; P:inflammatory response; TAS.
DR GO; GO:0008285; P:negative regulation of cell proliferation; TAS.
DR InterPro; IPR000827; CC_chemkine_sml.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
KW 3D-structure; Alternative splicing; Chemotaxis; Cytokine;
KW direct protein sequencing; Heparin-binding; Inflammatory response;
KW Polymorphism; Signal.
FT SIGNAL 1 21
FT CHAIN 22 120 Small inducible cytokine A23.
FT DISULFID 54 78
FT DISULFID 55 94
FT DISULFID 65 105
FT VARSPPLIC 46 46
FT VARIANT 106 106
FT CONFLICT 12 44
FT STRAND 58 58
FT HELIX 65 67
FT STRAND 70 73
FT TURN 76 77
FT STRAND 83 86
FT TURN 88 89
FT STRAND 92 95
FT TURN 97 98
FT HELIX 100 109
FT TURN 113 115
SQ SEQUENCE 120 AA; 13443 MW; 6CA622DD3A4B27AD CRC64;

Query Match 40.0%; Score 201.5; DB 1; Length 120;
Best Local Similarity 38.7%; Pred. No. 5.2e-15;
Matches 43; Conservative 22; Mismatches 25; Indels 21; Gaps 4;

Qy 1 MKISVAIPIFFLLITIALGKTSSS---SRGP-----YH--PSBCCFTYT 40
Db 1 MKVSVAALSCMLVT-ALGSAQRTKDAETEFMMSKLPLENVLLDRFHATSADCCISYT 59

Qy 41 TYKIPRIMDYETNSQCSKPGVITIKRGHSVCTNPSPDKWQDYIKDMK 91
Db 60 PRSIPCSLLESYPETNSQCSKPGVITLTKGRRCANFSPDKQVQCMRLK 110

RESULT 28
Q91265 ID Q91265 PRELIMINARY; PRT; 92 AA.
AC 091265;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE Macrophage inflammatory protein-1 alpha.
GN Name=MIP1 alpha;
OS Sigmodon hispidus (Hispid cotton rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
OC Sigmodon.

Query Match 39.1%; Score 197; DB 2; Length 88;
Best Local Similarity 40.4%; Pred. No. 1.2e-14;
Matches 40; Conservative 19; Mismatches 22; Indels 18; Gaps 3;

Qy 1 MKISVAIPIFFLLITIAL-----GKTESSSRGPVHPSECCFTYTYTKIPRIMDYE 54
```

```
OX NCBI_TaxID=42415;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=14980081; DOI=10.1089/107999004772719873;
RA Blanco J.C., Pletneva L., Boukhalova M., Richardson J.V.,
RA Harris K.A., Prince G.A.;
RT "the cotton rat: an underutilized animal model for human infectious
RT diseases can now be exploited using specific reagents to cytokines,
RT chemokines, and interferons.";
RL J. Interferon Cytokine Res. 24:21-28(2004).
DR EMBL; AY059407; AAL26704.1; -.
DR HSPB; P10147; I150.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008009; F:chemokine activity; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR Pfam; PF00048; IL8; 1.
DR SMART; SM00199; SCY; 1.
DR PROSITE; PS00472; SMALL_CYTOKINES_CC; UNKNOWN 1.
SQ SEQUENCE 92 AA; 10334 MW; CF9AAB3D94DCAF73 CRC64;

Query Match 39.5%; Score 199; DB 2; Length 92;
Best Local Similarity 43.0%; Pred. No. 7.6e-15;
Matches 40; Conservative 19; Mismatches 32; Indels 2; Gaps 2;

Qy 1 MKISVAIPIFFLLITIALGKTSSSRGPVHPSECCFTYTYTKIPRIMDYETNSQCS 60
Db 1 MKVPTAVLAVLLCI-ITLCNQVFSAPYGADTPTFCFSYGR-QIPRKFIADYFQTSLS 58

Qy 61 KPGVITIKRGHSVCTNPSPDKWQDYIKDMKEN 93
Db 59 EPGLIPLTKRRHVCADPKETWQVEIITDELN 91

RESULT 29
Q8HYP8 ID Q8HYP8 PRELIMINARY; PRT; 88 AA.
AC 08HYP8;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DE Chemokine CCL18/PARC.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22123042; PubMed=12126650; DOI=10.1006/cyto.2002.0875;
RA Basu S., Schaefer T.M., Ghosh M., Fuller C.L., Reinhart T.A.;
RT "Molecular cloning and sequencing of 25 different rhesus macaque
RT chemokine cDNAs reveals evolutionary conservation among C, CC, CX,
RT AND CX3C families of chemokines.";
RL Cytokine 18:140-148(2002).
DR EMBL; AF449272; AAN76076.1; -.
DR HSPB; P10147; I150.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008009; F:chemokine activity; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR002473; C-X-C/interkn_8.
DR InterPro; IPR000827; CC_chemkine_sml.
DR Pfam; PF00048; IL8; 1.
DR PRINTS; PR00436; INTERLEUKIN8.
DR SMART; SM00199; SCY; 1.
DR PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
SQ SEQUENCE 88 AA; 9797 MW; 19267D02F750D88F CRC64;

Query Match 39.1%; Score 197; DB 2; Length 88;
Best Local Similarity 40.4%; Pred. No. 1.2e-14;
Matches 40; Conservative 19; Mismatches 22; Indels 18; Gaps 3;

Qy 1 MKISVAIPIFFLLITIAL-----GKTESSSRGPVHPSECCFTYTYTKIPRIMDYE 54
```

```
Db      1  MKGLAAL--LVLCVALCSAQVTKKEP-----CCLVYTSRQIPQKFIVDYSE 48
Qy      55  TNSQCKPGIVFITKRGHSVCTNPSDKWQDYIKDMKEN 93
Db      49  TSPQCTKPGVILLKRRRQICADPNKKWQKYISDLKLN 87
```

## RESULT 30

```
SY05 RAT
ID _SY05_RAT STANDARD; PRT; 92 AA.
AC P50231;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Small inducible cytokine A5 precursor (CCL5) (T-cell specific RANTES
DE protein) (Sis-delta).
DE Name=Ccl5; Synonyms=Scya5;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
```

```
RP SEQUENCE FROM N.A.
RC STRAIN=Long Evans; TISSUE=Lung;
RA Jones M.L., Shanley T.P., Ward P.A.;
RL Submitted (FEB-1994) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Chemoattractant for blood monocytes, memory T helper
CC cells and eosinophils. Causes the release of histamine from
CC basophils and activates eosinophils (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the interleukin beta (chemokine CC) family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
```

```
CC -----
DR EMBL; U06436; AAA96499.1; -.
DR HSSP; P13501; IRTN.
DR RGD; 69069; Ccl5.
DR InterPro; IPR000827; CC chemokine sml.
DR InterPro; IPR001811; Chemokine_I18.
DR Pfam; PF00048; IL8; 1.
DR SMART; SM00199; SCY; 1.
DR PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
KW Chemotaxis; Cytokine; Inflammatory response; Signal; T-cell.
FT SIGNAL 1 24 Potential.
FT CHAIN 25 92 Small inducible cytokine A5.
FT DISULFID 34 58 By similarity.
FT DISULFID 35 74 By similarity.
SQ SEQUENCE 92 AA; 10170 MW; B4FBE2B4208ABC6 CRC64;
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Query Match 38.6%; Score 194.5; DB 1; Length 92;
Best Local Similarity 42.7%; Pred. No. 2.5e-14;
Matches 38; Conservative 15; Mismatches 31; Indels 5; Gaps 2;
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Qy      1  MKISVAIPFLIITIALGKTSSSRGPY--HPSECCFTYTYTKIPRQIMDYETNSQ 58
Db      1  MKISAAASLTIVLVAALCTVPAS---PYGSDTTPCCFAYLSIALPRAHVKEYFYTSSK 57
Qy      59  CSKPGIVFITKRGHSVCTNPSDKWQDYI 87
Db      58  CSNLAVFVTRNRQVCANPEKKWQDYI 86
```

Search completed: September 19, 2005, 08:57:36  
Job time : 177 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 19, 2005, 08:48:11 ; Search time 39 Seconds  
(without alignments)  
229,440 Million cell updates/sec

Title: US-10-626-530-2

Perfect score: 504

Sequence: 1 MKISVAIPFLITIALGT.....VCTNPDKWQDYIKDKMEN 93

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

1: PIR\_79:\*

2: Pirl:\*

3: Pirl3:\*

4: Pirl4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	240.5	47.7	93	2 B35673	LD78-beta protein
2	236	46.8	92	2 A30574	macrophage inflam
3	234.5	46.5	92	2 C30552	macrophage inflam
4	230.5	45.7	92	2 I46730	immune activation
5	224.5	44.5	92	1 A31767	macrophage inflam
6	223	44.2	92	2 A32393	macrophage inflam
7	223	44.2	92	2 I52322	macrophage inflam
8	191	37.9	91	1 A28815	monocyte chemoatr
9	189	37.5	91	1 A46539	monocyte chemoatr
10	183.5	36.4	120	2 J50177	lymphocyte and mon
11	180	35.7	116	2 I49555	gene C10 protein -
12	163	32.3	50	2 C60407	monocyte adherence
13	156	31.0	125	2 I46857	monocyte chemoatr
14	153.5	30.5	99	2 JC2136	monocyte chemoatr
15	151	30.0	99	2 JC5295	monocyte chemoatr
16	150.5	29.9	148	1 A30209	PDGF-inducible JB
17	149	29.6	148	1 S07723	immediate-early se
18	148.5	29.5	99	1 A39296	monocyte chemoatr
19	148.5	29.5	99	2 JC2336	monocyte chemoatr
20	146	29.0	109	2 A54678	monocyte chemoatr
21	144	28.6	99	2 JC2417	monocyte chemoatr
22	143	28.4	97	2 JC4912	eotaxin precursor
23	135.5	26.9	96	2 JC2478	eotaxin precursor
24	135.5	26.9	96	2 I48099	eotaxin precursor
25	127	25.2	99	2 A60299	monocyte chemoatr
26	126	25.0	120	2 I48147	monocyte chemoatr
27	123	24.4	95	2 A37236	I-309 protein prec
28	123	24.4	97	2 A48093	monocytic cytokine
29	122	24.2	72	2 A55984	monocyte chemoatr

30	116	23.0	114	1	ETHUL
31	93	18.5	114	1	ETMSL
32	86.5	17.2	92	2	S24236
33	85	16.9	101	2	I46871
34	82	16.3	101	2	I42496
35	81	16.1	103	2	A53096
36	79	15.7	95	2	JN0841
37	77.5	15.4	103	2	A26736
38	75.5	15.0	103	2	I50417
39	74	14.7	101	2	I48148
40	73	14.5	113	2	JC7800
41	69	13.7	99	2	A37034
42	69	13.7	117	2	B44253
43	69	13.7	4488	1	RRIMW2
44	68.5	13.6	311	2	T23873
45	68.5	13.6	316	2	H90372
46	67.5	13.4	1379	2	T13718
47	66.5	13.2	476	1	SGMSV
48	66	13.1	942	2	TL9553
49	65.5	13.0	703	2	S08119
50	65.5	13.0	704	2	A26125
51	65	12.9	348	2	T03911
52	64	12.7	114	2	A55010
53	64	12.7	128	2	T15101
54	64	12.7	573	2	T49610
55	63.5	12.6	208	2	B83773
56	63.5	12.6	461	1	A35356
57	63	12.5	184	2	B72168
58	63	12.5	184	2	T28578
59	63	12.5	184	2	A36852
60	63	12.5	501	1	A60005
61	63	12.5	501	1	VGEBMB
62	63	12.5	505	1	VGEBMH
63	62.5	12.4	496	2	T42562
64	62	12.3	100	2	I55614
65	62	12.3	100	2	S21467
66	62	12.3	107	2	JH0281
67	62	12.3	107	2	A28414
68	62	12.3	182	2	C90429
69	62	12.3	501	1	VGEBMA
70	62	12.3	808	2	E64492
71	61.5	12.2	101	2	B28414
72	61.5	12.2	302	2	A70711
73	61.5	12.2	336	2	H69069
74	61.5	12.2	593	2	T20630
75	61.5	12.2	703	2	A44983
76	61	12.1	104	2	T30750
77	61	12.1	126	2	A35766
78	61	12.1	1732	2	T14039
79	60.5	12.0	164	2	C35216
80	60.5	12.0	207	2	S25990
81	60.5	12.0	234	2	AD0486
82	60.5	12.0	293	2	T09065
83	60.5	12.0	450	2	S15675
84	60.5	12.0	682	2	A35969
85	60	11.9	113	2	S06547
86	60	11.9	308	2	T29756
87	60	11.9	422	2	B31776
88	60	11.9	557	2	T22079
89	59.5	11.8	257	2	B81155
90	59.5	11.8	257	2	C81949
91	59.5	11.8	286	2	AD0523
92	59.5	11.8	311	2	T52312
93	59.5	11.8	347	2	T07108
94	59.5	11.8	411	2	T07806
95	59.5	11.8	527	2	F97197
96	59.5	11.8	611	2	G90542
97	59.5	11.8	702	2	C86268
98	59.5	11.8	934	2	T39941
99	59.5	11.8	982	2	S58881
100	59	11.7	90	2	S69133

lymphotactin precu  
lymphotactin - mou  
TCA3 protein - mou  
interleukin-8 - ra  
interleukin-8 prec  
interleukin-8 prec  
interleukin-8 - do  
transformation-ind  
RSV-induced protei  
Neutrophil attract  
neutrophil activat  
interleukin-8 prec  
alveolar macrophag  
genome polyprotein  
hypothetical prote  
catechol 2,3-dioxy  
pollux gene protei  
vitronectin precur  
hypothetical prote  
heat shock protein  
heat shock protein  
r40cl protein - ri  
neutrophil-activat  
hypothetical prote  
related to rna bin  
hypothetical prote  
tumor necrosis fac  
A37R protein - var  
8R protein - vario  
A36R protein - var  
glycoprotein A pre  
glycoprotein A pre  
glycoprotein gp57-  
host shutoff virio  
macrophage inflam  
macrophage inflam  
macrophage inflam  
melanoma growth-st  
hypothetical prote  
hypothetical A pre  
glycoprotein A pre  
growth-regulated p  
hypothetical prote  
potassium channel  
hypothetical prote  
heat shock protein  
chemokine homolog  
platelet factor 4,  
protein kinase (EC  
FPI8 protein - low  
hypothetical prote  
probable exported  
hypothetical prote  
globulin-2 precurs  
heparin-binding gr  
finger protein (cl  
hypothetical prote  
hypothetical prote  
conserved hypothet  
hypothetical prote  
spermidine synthas  
deacetoxycephalos  
glucan endo-1,3-be  
acyl-lacyl-carrier  
uncharacterized co  
gtp-binding protei  
F13B4.2 protein -  
hypothetical prote  
mutS protein homol  
platelet factor 4





F;1-23/Domain: signal sequence #status predicted <SIG>  
F;24-92/Product: macrophage inflammatory protein 1-beta #status experimental <MAT>  
F;34-58,35-74/Disulfide bonds: #status experimental

Query Match 44.5%; Score 224.5; DB 1; Length 92;  
Best Local Similarity 43.0%; Pred. No. 9.7e-18;  
Matches 40; Conservative 20; Mismatches 32; Indels 1; Gaps 1;

QY 1 MKISVAAPFFLLITLALGTKTSSSRGPHSECCFTYTKIPRQIMDYETNSQCS 60  
DB 1 MKLCVTLSLLMLVA-AFCSPALSWPGSDPPACCFSTARKLPKNFVVDYIETSSLCS 59

QY 61 KPGIVFTRKSHSVCTNPSPDKWQYIKDMKEN 93

DB 60 QPAVVFQTKRSQKQVCADPSSEWQEVYIDLELN 92

RESULT 6

A;Molecule type: DNA  
A;Residues: 1-92 <RES>  
A;Cross-references: GB:M73061; NID:g199694; PIDN:AAA39707.1; PID:g199695  
C;Comment: This protein is a monokine.  
C;Genetics:  
A;Introns: 23/3; 26/1; 63/2  
C;Superfamily: macrophage inflammatory protein  
C;Keywords: heparin binding  
F;1-23/Domain: signal sequence #status predicted <SIG>  
F;24-92/Product: macrophage inflammatory protein #status experimental <MAT>

Query Match 44.2%; Score 223; DB 2; Length 92;  
Best Local Similarity 45.2%; Pred. No. 1.4e-17;  
Matches 42; Conservative 21; Mismatches 28; Indels 2; Gaps 2;  
QY 1 MKISVAAPFFLLITLALGTKTSSSRGPHSECCFTYTKIPRQIMDYETNSQCS 60  
DB 1 MKVSTALAA-VLLCTMTLNCQVFSAPYGDATPTACCFYSR-KIPRQFIVDYFETSSLCS 58  
QY 61 KPGIVFTRKSHSVCTNPSPDKWQYIKDMKEN 93  
DB 59 QPGVIFLTRNRQICADSKETWQVEYITDLELN 91  
RESULT 7  
I52322  
macrophage inflammatory protein-l-alpha - rat  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 09-Jul-2004  
C;Accession: I52322  
R;Shi, M.M.; Godleski, J.J.; Paulauskis, J.D.  
Biochem. Biophys. Res. Commun. 211, 289-295, 1995  
A;Title: Molecular cloning and posttranscriptional regulation of macrophage inflammatory protein  
A;Reference number: I52322; MUID:95298037; PMID:7779098  
A;Accession: I52322  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-92 <RES>  
A;Cross-references: UNIPROT:P50229; EMBL:U22414; NID:g790632; PIDN:AAA0608.1; PID:g79063  
C;Superfamily: macrophage inflammatory protein  
Query Match 44.2%; Score 223; DB 2; Length 92;  
Best Local Similarity 45.2%; Pred. No. 1.4e-17;  
Matches 42; Conservative 22; Mismatches 27; Indels 2; Gaps 2;  
QY 1 MKISVAAPFFLLITLALGTKTSSSRGPHSECCFTYTKIPRQIMDYETNSQCS 60  
DB 1 MKVSTALAA-VLLCTMTLNCQVFSAPYGDATPTACCFYSR-QIPRKFADYFETSSLCS 58  
QY 61 KPGIVFTRKSHSVCTNPSPDKWQYIKDMKEN 93  
DB 59 QPGVIFLTRNRQICADSKETWQVEYITDLELN 91  
RESULT 8  
A28815  
monocyte chemoattractant cytokine RANTES precursor - human

F;1-23/Domain: signal sequence #status predicted <SIG>  
F;24-92/Product: macrophage inflammatory protein 1-beta #status experimental <MAT>  
F;34-58,35-74/Disulfide bonds: #status experimental  
Query Match 44.5%; Score 224.5; DB 1; Length 92;  
Best Local Similarity 43.0%; Pred. No. 9.7e-18;  
Matches 40; Conservative 20; Mismatches 32; Indels 1; Gaps 1;  
QY 1 MKISVAAPFFLLITLALGTKTSSSRGPHSECCFTYTKIPRQIMDYETNSQCS 60  
DB 1 MKLCVTLSLLMLVA-AFCSPALSWPGSDPPACCFSTARKLPKNFVVDYIETSSLCS 59  
QY 61 KPGIVFTRKSHSVCTNPSPDKWQYIKDMKEN 93  
DB 60 QPAVVFQTKRSQKQVCADPSSEWQEVYIDLELN 92  
RESULT 6  
macrophage inflammatory protein-1-alpha precursor - mouse  
N;Alternate names: heparin-binding chemotaxis protein; L2G25B protein; SC1/MIP-1a; SIS a  
C;Species: Mus musculus (house mouse)  
C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 09-Jul-2004  
C;Accession: S11685; A32393; S04533; A53885; A30552; PS0303; A27596; I56104  
R;Grove, M.; Lowe, S.; Graham, G.; Pragnelli, I.; Plumb, M.  
Nucleic Acids Res. 18, 5561, 1990  
A;Title: Sequence of the murine haemopoietic stem cell inhibitor/macrophage inflammatory protein  
A;Reference number: S11685; MUID:91016858; PMID:2216738  
A;Accession: S11685  
A;Molecule type: DNA  
A;Residues: 1-92 <GRO>  
A;Cross-references: UNIPROT:P10855; EMBL:X53372; NID:g54062; PIDN:CAA37452.1; PID:g29753  
A;Note: the authors' translation of the nucleotide sequence differs at several positions  
R;Kwon, B.S.; Weisman, S.M.  
Proc. Natl. Acad. Sci. U.S.A. 86, 1963-1967, 1989  
A;Title: cDNA sequence of two inducible T-cell genes.  
A;Reference number: A32393; MUID:89184547; PMID:2784565  
A;Accession: A32393  
A;Molecule type: mRNA  
A;Residues: 1-92 <KWO>  
A;Cross-references: GB:J04491; NID:g201524; PIDN:AAA40304.1; PID:g201525  
R;Davatelis, G.; Tekamp-Olson, P.; Wolpe, S.D.; Hermesen, K.; Luedke, C.; Gallegos, C.; C  
J. Exp. Med. 167, 1939-1944, 1988  
A;Title: Cloning and characterization of a cDNA for murine macrophage inflammatory prote  
A;Reference number: S04533; MUID:88258380; PMID:3290382  
A;Accession: S04533  
A;Molecule type: mRNA  
A;Residues: 1-48, 'E', 50-90, 'I', 92 <DA2>  
A;Cross-references: EMBL:X12531  
A;Note: the authors translated the codon GAG for residue 49 as Asp and ATT for residue 9  
A;Title: The sequence has been corrected in reference A53885  
R;Davatelis, G.; Tekamp-Olson, P.; Wolpe, S.D.; Hermesen, K.; Luedke, C.; Gallegos, C.; C  
J. Exp. Med. 170, 2189, 1989  
A;Reference number: A53885  
A;Contents: erratum  
A;Accession: A53885  
A;Molecule type: mRNA  
A;Residues: 1-92 <DAV>  
A;Cross-references: EMBL:X12531; NID:g53122; PIDN:CAA31047.1; PID:g53123  
R;Brown, K.D.; Zurawski, S.M.; Mosmann, T.R.; Zurawski, G.  
J. Immunol. 142, 679-687, 1989  
A;Title: A family of small inducible proteins secreted by leukocytes are members of a ne  
s of various activation processes.  
A;Reference number: A30552; MUID:89093958; PMID:2521353  
A;Accession: A30552  
A;Molecule type: mRNA  
A;Residues: 1-21, 'L', 23-61, 'A', 63-92 <BRO>  
A;Cross-references: GB:M23447; NID:g533240; PIDN:AAA40146.1; PID:g533241  
R;Sherry, B.; Tekamp-Olson, P.; Gallegos, C.; Bauer, D.; Davatelis, G.; Wolpe, S.D.; Ma  
J. Exp. Med. 168, 2251-2259, 1988  
A;Title: Resolution of the two components of macrophage inflammatory protein 1, and clon  
A;Reference number: JLO088; MUID:89067830; PMID:3058856  
A;Accession: PS0303

N;Alternate names: small inducible cytokine A5; T-cell specific cytokine RANTES  
C;Species: Homo sapiens (man)  
C;Date: 30-Jun-1989 #sequence\_revision 16-Aug-1996 #text\_change 09-Jul-2004  
C;Accession: A28815  
R;Schall, T.J.; Jongstra, J.; Dyer, B.J.; Jorgensen, J.; Clayberger, C.; Davis, M.M.; Kr  
J. Immunol. 141, 1018-1025, 1988  
A;Title: A human T cell-specific molecule is a member of a new gene family.  
A;Reference number: A28815; MUID:88285659; PMID:2456327  
A;Accession: A28815  
A;Molecule type: mRNA  
A;Residues: 1-91 <SCH>  
A;Cross-references: UNIPROT:P13501; GB:M21121  
C;Comment: The acronym RANTES reflects the description "Regulated upon Activation, Norma  
C;Genetics:  
A;Gene: GDB:SCYA5; D17S136E  
A;Cross-references: GDB:120749; OMIM:187011  
A;Map position: 17q11.2-17q12  
C;Superfamily: macrophage inflammatory protein  
C;Keywords: chemotaxis; cytokine; immediate-early protein; inflammation; T-cell  
F;1-23/Domain: signal sequence #status predicted <Sig>  
F;24-91/Product: T-cell protein RANTES #status predicted <MAT>  
Query Match 37.9%; Score 191; DB 1; Length 91;  
Best Local Similarity 36.6%; Pred. No. 4.9e-14;  
Matches 34; Conservative 18; Mismatches 35; Indels 6; Gaps 2;  
QY 1 MKISVAAIPFLLITLITGKTSSSRGPY--HPSECCFTYTYKIPRQIMDYETNSQ 58  
DB 1 MKVSAALAVLILATLCA---PASASPYSSDTPCCFAYIARPLPRAHKEYFYTSKG 56  
QY 59 CSKPGIVFITKRGHVSVCNTPSDKWQDYIKDMK 91  
DB 57 CSNPAAVVFVTRKQRCVCAPEKKWVREYINSLE 89  
RESULT 9  
A46539  
monocyte chemoattractant cytokine RANTES precursor - mouse  
N;Alternate names: MuRantes  
C;Species: Mus musculus (house mouse)  
C;Date: 18-Jun-1993 #sequence\_revision 16-Aug-1996 #text\_change 09-Jul-2004  
C;Accession: I48875; A46539; I48654; I56970  
R;Danoff, T.M.; Kallay, P.A.; Chang, Y.S.; Heeger, P.S.; Neilson, E.G.  
J. Immunol. 152, 1182-1189, 1994  
A;Title: Cloning, genomic organization, and chromosomal localization of the Scya5 gene  
A;Reference number: I48875; MUID:94132613; PMID:7507961  
A;Accession: I48875  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-91 <DAN>  
A;Cross-references: UNIPROT:P30882; EMBL:U02298; NID:9460090; PIDN:AAA18302.1; PID:g4600  
R;Schall, T.J.; Simpson, N.J.; Mak, J.Y.  
Eur. J. Immunol. 22, 1477-1481, 1992  
A;Title: Molecular cloning and expression of the murine RANTES cytokine: structural and  
A;Reference number: A46539; MUID:92289805; PMID:1376260  
A;Accession: A46539  
A;Molecule type: mRNA  
A;Residues: 1-18, 'A', 20-91 <SCH>  
A;Cross-references: GB:G37648; NID:g250207; PIDN:AAB22330.1; PID:g250208  
A;Experimental source: macrophage cell line PUS-1.8  
A;Note: Sequence extracted from NCBI backbone (NCBIN:106768, NCBI:P106770)  
R;Shin, H.S.; Drysdale, B.E.; Shin, M.L.; Noble, P.W.; Fisher, S.N.; Paznekas, W.A.  
Mol. Cell. Biol. 14, 2914-2925, 1994  
A;Title: Definition of a lipopolysaccharide-responsive element in the 5'-flanking region  
A;Reference number: I48654; MUID:94217689; PMID:7513046  
A;Accession: I48654  
A;Status: translation not shown; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-91 <SHI>  
A;Cross-references: EMBL:X70675; NID:g475205; PIDN:CAA50011.1; PID:g475206  
R;Neilson, E.G.; Krensky, A.  
Kidney Int. 41, 220-225, 1992  
A;Title: Isolation and characterization of cDNA from renal tubular epithelium encoding m

A;Reference number: I56970; MUID:92277990; PMID:1375672  
A;Accession: I56970  
A;Status: translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-40, 'E', 42-91 <NET>  
A;Cross-references: GB:M77747; NID:g200649; PIDN:AAA40029.1; PID:g200650  
C;Comment: This chemoattractant for monocytes but not neutrophils is an immediate-early  
C;Genetics:  
A;Introns: 26/1; 63/2  
A;Superfamily: macrophage inflammatory protein  
C;Keywords: chemotaxis; cytokine; immediate-early protein; inflammation  
F;1-23/Domain: signal sequence #status predicted <Sig>  
F;24-91/Product: monocyte chemoattractant cytokine RANTES #status predicted <MAT>  
Query Match 37.5%; Score 189; DB 1; Length 91;  
Best Local Similarity 42.7%; Pred. No. 8.2e-14;  
Matches 38; Conservative 15; Mismatches 30; Indels 6; Gaps 3;  
QY 1 MKISVAAIPFLLITLITGKTSSSRGPY--HPSECCFTYTYKIPRQIMDYETNSQ 58  
DB 1 MKISAAALT-IILTAALCTPAPAS---PYGSDTTPCCFAYLSLALPRAHKEYFYTSK 56  
QY 59 CSKPGIVFITKRGHVSVCNTPSDKWQDYI 87  
DB 57 CSNLAVVVFVTRNRQVCANPEKKWQVEYI 85  
RESULT 10  
JE0177  
lymphocyte and monocyte chemoattractant CC chemokine - human  
C;Species: Homo sapiens (man)  
C;Date: 10-Jul-1998 #sequence\_revision 10-Jul-1998 #text\_change 17-Mar-1999  
C;Accession: JE0177  
R;Youn, B.S.; Zhang, S.; Broxmeyer, H.E.; Antol, K.; Fraser Jr., M.J.; Hangoc, G.; Kwon,  
Biochem. Biophys. Res. Commun. 247, 217-222, 1998  
A;Title: Isolation and characterization of LMC, a novel lymphocyte and monocyte chemoat  
A;Reference number: JE0177; MUID:98308096; PMID:9642106  
A;Accession: JE0177  
A;Molecule type: mRNA  
A;Residues: 1-120 <YOU>  
Query Match 36.4%; Score 183.5; DB 2; Length 120;  
Best Local Similarity 42.4%; Pred. No. 4.4e-13;  
Matches 39; Conservative 15; Mismatches 33; Indels 5; Gaps 3;  
QY 1 MKISVAAIPFLLITLITGKTSSSRGPY---YHPSECCFTYTYKIPRQIMDYETNS 57  
DB 1 MKVSEAAALSLVLLI-ITSASRSQKVPBWVWTPSTCCLKYYE-KVPLRLLVGVYKAL 58  
QY 58 QCSKPGIVFITKRGHVSVCNTPSDKWQDYIKD 89  
DB 59 NCHLPAIIFVTKRNRREVCTNPNDNDWQVEYIKD 90  
RESULT 11  
I49555  
gene C10 protein - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004  
C;Accession: I49555  
R;Orlowski, A.; Berger, M.S.; Prystowsky, M.B.  
Cell Regul. 2, 403-412, 1991  
A;Title: Novel expression pattern of a new member of the MIP-1 family of cytokine-like g  
A;Reference number: I49555; MUID:91370083; PMID:1832565  
A;Accession: I49555  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-116 <RES>  
A;Cross-references: UNIPROT:P27784; GB:M58004; NID:g192243; PIDN:AAA37329.1; PID:g192244  
C;Genetics:  
A;Gene: C10  
C;Superfamily: macrophage inflammatory protein

```
Query Match          35.7%; Score 180; DB 2; Length 116;
Best Local Similarity 37.6%; Pred. No. 1e-12;
Matches 41; Conservative 22; Mismatches 26; Indels 20; Gaps 5;

QY 1 MKISVAAPFFLLIITIALGKT-----SSSRGPHP-----SECCFTYTYVK 43
   ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 1 MRNSKTAISFTILVAV-LGSAGLIQEMEKEDR-RYNPPIIHQGFQDTSDDCCFSYAT-Q 57

QY 44 IPQRIMDYETNSQCSKSGIVFITKRGHVSCTNPSPDKWQDYIKDMKE 92
   ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 58 IPCKRFIYFPTSGGCIKPGIIFISRRGTQVCADPSDRRVQRCCLTLKQ 106

RESULT 12
C60407
monocyte adherence-induced protein 5 beta - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 06-Nov-1992 #sequence_revision 06-Nov-1992 #text_change 09-Jul-2004
C:Accession: C60407
R:Sporn, S.A.; Eierman, D.F.; Johnson, C.E.; Morris, J.; Martin, G.; Ladner, M.; Haskill
J.; Immunol. 144, 4434-4441, 1990
A:Title: Monocyte adherence results in selective induction of novel genes sharing homolo
A:Reference number: A60407; MUID:90257367; PMID:2341726
A:Accession: C60407
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-50 <SPO>
A:Cross-references: UNIPROT:Q8NHWA
C:Superfamily: macrophage inflammatory protein

Query Match          32.3%; Score 163; DB 2; Length 50;
Best Local Similarity 52.0%; Pred. No. 3.5e-11;
Matches 26; Conservative 12; Mismatches 12; Indels 0; Gaps 0;

QY 44 IPQRIMDYETNSQCSKSGIVFITKRGHVSCTNPSPDKWQDYIKDMKEN 93
   ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 1 VPRNFVVDYETSSLCQPAVVFTQKRSKQVCADPSSESWQEVYVDLELN 50

RESULT 13
I46857
monocyte chemoattractant protein-1 - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 09-Jul-2004
C:Accession: I46857
R:Yoshimura, T.; Yuhki, N.
J. Immunol. 146, 3483-3488, 1991
A:Title: Neutrophil attractant/activation protein-1 and monocyte chemoattractant protein
A:Reference number: I46857; MUID:91225489; PMID:2026877
A:Accession: I46857
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-125 <YOS>
A:Cross-references: UNIPROT:P28292; GB:M57440; NID:g165469; PIDN:AAA31386.1; PID:g165470
C:Superfamily: macrophage inflammatory protein

Query Match          31.0%; Score 156; DB 2; Length 125;
Best Local Similarity 35.2%; Pred. No. 5.1e-10;
Matches 32; Conservative 17; Mismatches 40; Indels 2; Gaps 2;

QY 1 MKISVAAPFFLLIITIALGKTSSSRGPHPSECCFTYTYKIPQRIMDYETNS-OC 59
   ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 1 MKVS-ATLLCLLLIAVAFSSHVLAQPDVAVNSPTCCYTCYTNKTSISKRLMSYRRINSTKC 59

QY 60 SKPGIVFITKRGHVSCTNPSPDKWQDYIKDM 90
   ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 60 PREAVIFMTKLAKGICADPKQKRWQDAIANL 90

RESULT 14
JC2136
monocyte chemoattractant protein-1 precursor - pig
C:Species: Sus scrofa domestica (domestic pig)
```

```
C:Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 09-Jul-2004
C:Accession: JC2136; S57498
R:Hosang, K.; Knoke, I.; Klaidiny, J.; Wempe, F.; Wuttke, W.; Scheit, K.H.
Biochem. Biophys. Res. Commun. 199, 962-968, 1994
A:Title: Porcine luteal cells express monocyte chemoattractant protein-1 (MCP-1): Analysis
A:Reference number: JC2136; MUID:94183284; PMID:7510962
A:Accession: JC2136
A:Molecule type: mRNA
A:Residues: 1-99 <HOS>
A:Cross-references: UNIPROT:P42831; GB:Z48479; NID:g683716; PIDN:CAA88370.1; PID:g683717
R:Zach, O.
submitted to the EMBL Data Library, July 1994
A:Reference number: S57497
A:Accession: S57498
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-99 <ZAC>
A:Cross-references: EMBL:X79416; NID:g872312; PIDN:CAAS5945.1; PID:g872313
C:Superfamily: macrophage inflammatory protein
C:Keywords: glycoprotein
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-99/Product: monocyte chemoattractant protein-1 #status predicted <MAT>
F:94/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match          30.5%; Score 153.5; DB 2; Length 99;
Best Local Similarity 37.9%; Pred. No. 7.6e-10;
Matches 36; Conservative 14; Mismatches 42; Indels 3; Gaps 3;

QY 1 MKISVAAPFFLLIITIALGKTSSSRGPHPSECCFTYTYKIPQRIMDYE-TNSOC 59
   ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 1 MKVS-AALLCLLLTAATFCTQLAQPDAINSPTCYTLTKSKISQRLMSYRRVTSSKC 59

QY 60 SKPGIVFITKRGHVSCTNPSPDKWQDYIKDM-KEN 93
   ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 60 PREAVIFKTIAGKEICAEKPKQKRWQDSISHLDDKN 94

RESULT 15
JC5295
monocyte chemotactic protein-2 precursor - human
C:Species: Homo sapiens (man)
C:Date: 02-May-1997 #sequence_revision 18-Jul-1997 #text_change 09-Jul-2004
C:Accession: JC5295
R:Van Coillie, E.; Froyen, G.; Nomiya, H.; Miura, R.; Fiten, P.; Van Aelst, I.; Van Dan
Biochem. Biophys. Res. Commun. 231, 726-730, 1997
A:Title: Human monocyte chemotactic protein-2: cDNA cloning and regulated expression of n
A:Reference number: JC5295; MUID:97224420; PMID:9070881
A:Accession: JC5295
A:Molecule type: mRNA
A:Residues: 1-99 <VAN>
A:Cross-references: UNIPROT:P80075; GB:Y10802; NID:g1924937; PIDN:CAA71760.1; PID:g192493
A:Experimental source: bone marrow
C:Comment: This protein belongs to the beta-chemokine family which is one of the major H
tis and in tumor biology, and contribute to the trafficking and recruitment of the respon
C:Genetics:
A:Gene: mcp-2
C:Superfamily: macrophage inflammatory protein
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-99/Product: monocyte chemotactic protein-2 #status predicted <MAT>

Query Match          30.0%; Score 151; DB 2; Length 99;
Best Local Similarity 35.5%; Pred. No. 1.4e-09;
Matches 33; Conservative 16; Mismatches 42; Indels 2; Gaps 2;

QY 1 MKISVAAPFFLLIITIALGKTSSSRGPHPSECCFTYTYKIPQRIMDYE-TNSOC 59
   ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 1 MKVS-AALLCLLLMAATFSPQGLAQPDVSVSIPITCCFNVINRKIPQIRLESYTRITIOC 59

QY 60 SKPGIVFITKRGHVSCTNPSPDKWQDYIKDMKE 92
   ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 60 PREAVIFKTQKGEVCAADPKERWVRDMSKHLQD 92
```

RESULT 16

A30209  
 A30209  
 PDGF-inducible JE glycoprotein precursor - mouse  
 C|Species: Mus musculus (house mouse)  
 C|Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text\_change 09-Jul-2004  
 C|Accession: A30209; A44771; A30861  
 R|Rollins, B.J.; Morrison, E.D.; Stiles, C.D.  
 Proc. Natl. Acad. Sci. U.S.A. 85, 3738-3742, 1988  
 A|Title: Cloning and expression of JE, a gene inducible by platelet-derived growth factor  
 A|Reference number: A30209; MUID:88234501; PMID:3287374  
 A|Accession: A30209  
 A|Molecule type: DNA  
 A|Residues: 1-148 <ROL>

A;Residues: 1-148 <ROL>  
A;Cross-references: UNIPROT:P10148; GB:M19681; NID:G193486; PTDN:AAA37684.1; PID:G387168  
R;Kawahara, R.S.: Deuel, T.F.

J;Kawabuchi K, Sato T, Ueda T, et al. 1989  
 J. Biol. Chem. 264, 679-682, 1989  
 A:Title: Platelet-derived growth factor-inducible gene JE is a member of a family of small  
 A:Reference number: A44771; MUID:89093129; PMID:2910858  
 A:Accession: A44771  
 A:Molecule type: DNA; mRNA  
 A:Residues: 1-148 <K2>  
 A:Cross-references: GB:J04467; NID:g193488; PIDN:AAA37685.1; PID:g9387169  
 C:Genetics:  
 A:Gene: JE

A; gene: 05  
A; introns: 26/1; 65/2  
C; Superfamily: macrophage inflammatory protein  
C; Keywords: cytokine; glycoprotein  
F; 126/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 29.9%; Score 150.5; DB 1; Length 148;  
Best Local Similarity 41.3%; Pred. No. 2.4e-09;  
Matches 26; Conservative 13; Mismatches 23; Indels 1; Gaps 1;

<b>Qy</b>	32 PSECFTYTYKIPIRIMDYB-TNSQSKPGIVFITKRGHSVCTNPDKWQDIKOM 90       : :     :     :     :     :     :
<b>D6</b>	31 PLTCYSFTSMIPMSLESKYRTSRSCKEAVFVKLRKVCCADPKKEWVOYIKNL 90       : :     :     :     :     :     :

09 91 KEN 93

— 01 02

## RESULT 17

S07723  
 R05021 17  
 immediate-early serum-responsive protein JE precursor - rat  
 N:Alternate names: monocyte chemoattractant protein-1  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004  
 C:Accession: S07723; JN0128  
 R:Timmers, H.T.M.; Pronk, G.J.; Bos, J.L.; van der Eb, A.J.  
 Nucleic Acids Res. 18, 23-34, 1990  
 A:Title: Analysis of the rat JE gene promoter identifies an AP-1 binding site essential  
 A:Reference number: S07723; MUID:90174947; PMID:2106664

A;Accession: S07723  
A;Accession: S07723  
A;Molecule type: DNA  
A;Residues: 1-148 <TIM>

A; Ks/resques: 1-148 <IM>  
A; Cross-references: UNIPROT:P14844; EMBL:X17053; NID:G55530; PIDN:CAA34901.1; PID:G55531  
R; Yoshimura, T.; Takeya, M.; Takahashi, K.  
D; Biochem Biophys Res Commun 174:504-509 1991

A:Title: Molecular cloning of rat monocyte chemoattractant protein-1 (MCP-1) and its expression in macrophages  
A:Reference number: JN0128; MUID:91128376; PMID:1704226

A: Accession: JN0128  
A: Molecule type: mRNA  
A: Residues: 1-148 <YOS>

A; Cross-references: GB:M57441; NID:g205333; PIDN:AAA63496.1; PID:g205334  
A; Experimental source: spleen cells  
A; Note: the authors translated the codon GAA for residue 62 as Lys and GCT for residue 63

C;Genetics:  
C;Notes: the amino acids translated the amino acid sequence of the protein  
C;A:Introns: 26/1; 65/2  
C;Superfamily: macrophage inflammatory protein

C; Superfamily: macrophage inflammatory protein  
F; 1-23/Domain: signal sequence #status predicted <SIG>  
F; 24-148/Product: immediate-early serum-responsive protein JE #status predicted <WAT>

## Query M:

Query Match 23.0%; Occid. 145; Length 110;  
Best Local Similarity 33.7%; Pred. NO. 3.6e-09;  
Matches 32; Conservative 20; Mismatches 39; Indels

**Qy**            1 MKISVAAIPIFFELLITI-ALGKTSSSRGPYHPSECCFTYTYKIPRORIMDYVE-TNSQ 58  
              | : | | : | | | : | | | : | | | : | | | : | | : | | :  
**D6**            1 MQVSVTLIG--LLFTVAACSIHVLSODDAVNAPLTCYSFSGTGNIPMSLENYKRITSSR 58  
              | : | | : | | | : | | | : | | | : | | | : | | : | | :

59 CSKPGIVFITRGHSVCTNPSPDKWVQDYIKDMKEN 93

59 CPKEAVFVTKLKREICADPNKEVWQYIRKLDQN 93

RESULT 18

Accession: A39296  
 N:Alternate names: monocyte chemoattractant protein 1 precursor - bovine  
 C:Species: Bos primigenius taurus (cattle)  
 C>Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #translation\_revision 10-Sep-1999  
 C:Accession: A39296  
 R:Wempe, F.; Henschen, A.; Scheit, K.H.  
 DNA Cell Biol. 10, 671-679, 1991  
 A>Title: Gene expression and cDNA cloning identified  
 A:Reference number: A39296; MUID:32096117; PMID:172181  
 A:Accession: A39296

A:Accession: A39258  
A:Molecule type: mRNA  
A:Residues: 1-99 <WEM>  
A:Cross-references: UNIPROT:P28291; GB:M84602; GB:M85  
A:Accession: B39296

A: Molecule type: protein  
 A: Residues: 50-68, 'X', 70-74, 'X', 75 <WE2>  
 A: Experimental source: seminal vesicle  
 C: Superfamily: macrophage inflammatory protein  
 C: Keywords: glycoprotein  
 P: 1-23/Domain; signal sequence #status predicted -SIG  
 P: 24-99/Product; monocyte chemoattractant protein 1 #sta  
 P: 94/Binding site; carboxylate (Asp) (covalent) #sta

Query Match 29.5%; Score 148.5; DB 1; Length 99;  
Best Local Similarity 36.8%; Pred. No. 2.7e-09;  
Matches 35: Conservative 17; Mismatches 40; Indels

[illegible]

DB I MKVS-AAALTCTLELIVAAAFSTIEVLAQPDAINSQVACCYI

QV 60 SKPGIVEITKRGHSVCTNPSPDKWVDYIKDM-KEN 93

QY	60	SAPGIVFIIKRGHSVCINFESDRAWVQDIIDKW-KEN	93
		: :     :   :   :   :   :   :	
pB	60	PKEAVIFKTLIGKELCADEPKOKWVODPSINYLNKK	94

DEPT. T 19

monocyte chemoattractant protein-1 - bovine  
C/Species: Bos primigenius indicus (zebu cattle)  
C/Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 0  
C/Accession: JJC2336

R;Wempe, F.; Kuhlmann, J.K.; Scheit, K.H.  
Biochem. Biophys. Res. Commun. 202, 1272-1279, 1994  
A;Title: Characterization of the bovine monocyte chemoattractant protein-1 gene.  
A;Reference number: JC2336; MUID:94338337; PMID:8060303  
A;Accession: JC2336  
A;Molecule type: protein  
A;Residues: 1-99 <WEM>

A;Residues: 1-99 <MEM>  
C;Genetics:  
A;Gene: MCP-1  
A;Introns: 26/1; 65/2  
C;Superfamily: macrophage inflammatory protein

Query Match	29.5%	Score 148.5;	DB 2;	Length 99;
Best Local Similarity	36.8%;	Pred. No. 2.7e-09;		
Matches 35: Conservative	17: Mismatches	40: Indels	3: Gaps	3:









```

C;Comment: It has not yet been shown that the previously detected eosinophilotoxic pept
C;Genetics:
A;Gene: GDB:SCVCL1; LTN; LPTN; ATAC
A;Cross-references: GDB:682094
A;Map position: lq23-lq25
C;Superfamily: lymphotactin
C;Keywords: chemotaxis; cytokine; lymphokine; mast cell; T-cell
F;1-15/Domain: signal sequence #status predicted <SIG>
F;16-21/Domain: propeptide #status predicted <PRO>
F;22-114/Product: lymphotactin #status predicted <MAT>
F;22-25/Product: eosinophilotoxic peptide #status predicted <EOP>
F;32-69/Disulfide bonds: #status predicted

Query Match      23.0%; Score 116; DB 1; Length 114;
Best Local Similarity 31.5%; Pred No. 1.2e-05;
Matches 29; Conservative 18; Mismatches 35; Indels 10; Gaps 3;

Qy  1 MKISVAIRPFLLIT--IALGKTKESSRGYPHPSECCFTYTYKIPRORIMDYETNSQ 58
Db  1 MRLILALLGTCSTAYIVEGVSEVSK-----RTCVSLTQRLPVSRIKTY--TIE 52

Qy  59 CSKPGVIFITKRGHSVCTNPSDKWQDYIKM 90
Db  53 GSLRAVIFITKRLKVKCADPQATWTRDVVRSM 84

Search completed: September 19, 2005, 08:58:21
Job time : 42 secs

```

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 19, 2005, 08:44:26 ; Search time 165 Seconds  
(without alignments)  
217.992 Million cell updates/sec

Title: US-10-626-530-2

Perfect score: 504

Sequence: 1 MKTSVAIPFLITLITLGT.....VCTNPSDKWQYIKDMKEN 93

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : A Geneseq\_16Dec04:\*

1: Geneseqp1980s:\*

2: Geneseqp1990s:\*

3: Geneseqp2000s:\*

4: Geneseqp2001s:\*

5: Geneseqp2002s:\*

6: Geneseqp2003as:\*

7: Geneseqp2003bs:\*

8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	504	100.0	93	2	AAR76128 Macrophag
2	504	100.0	93	2	AAR95691 Pituitary
3	504	100.0	93	2	AAW07203 Human MIP
4	504	100.0	93	2	AAW38171 Human che
5	504	100.0	93	2	AAW57697 Human M-C
6	504	100.0	93	3	AB27659 Human pro
7	504	100.0	93	3	AB15806 Human che
8	504	100.0	93	4	AB68294 Amino aci
9	504	100.0	93	4	AB50992 Human PRO
10	504	100.0	93	5	AB90773 Human Tum
11	504	100.0	93	5	AB90774 Human Tum
12	504	100.0	93	5	AB90772 Human Tum
13	504	100.0	93	6	ABU61834 Chemokine
14	504	100.0	93	6	ABU61832 Human MIP
15	504	100.0	93	6	ABU61833 Pituitary
16	504	100.0	93	6	ABU54479 Human nor
17	504	100.0	93	6	ABU54481 Human nor
18	504	100.0	93	6	ABU54480 Human nor
19	504	100.0	93	6	ABP76018 Human GEN
20	504	100.0	93	7	ADD06466 Human Ckb
21	504	100.0	93	7	ADFI15213 Human alb
22	504	100.0	93	7	ADFI16716 Human alb
23	504	100.0	93	7	ADFI16713 Human alb
24	504	100.0	93	7	ADFI16715 Human alb
25	504	100.0	93	7	ADFI15205 Human alb

Adfi15332 Human alb  
Adfi16667 Human alb  
Adfi16714 Human alb  
Adfi16739 Human alb  
Adfi15204 Human alb  
Adfi15208 Human alb  
Adfi15209 Human alb  
Adfi15224 Human alb  
Adfi15309 Human alb  
Adfi15326 Human alb  
Adfi16712 Human alb  
Adfi16686 Human alb  
Adfi16694 Human alb  
Abu61831 Macrophag  
Aaw38172 Human che  
Aaw82723 Human CCC  
Adn04138 Antipiori  
Aaw52843 Human mat  
Aar77600 Human cir  
Aab68295 Amino aci  
Aao20020 Human che  
Aao14153 Human HCC  
Aao21107 HCC1 chem  
Aao21097 Protein o  
Adfi16638 Human alb  
Adfi16641 Human alb  
Adfi16640 Human alb  
Adfi16636 Human alb  
Adfi16637 Human alb  
Adfi16634 Human alb  
Adfi16642 Human alb  
Adfi16635 Human alb  
Adfi16633 Human alb  
Adfi16639 Human alb  
Add06557 Human Ckb  
Add06554 Human Ckb  
Adfi14991 Human alb  
Adfi14990 Human alb  
Add06556 Human Ckb  
Add06553 Human Ckb  
Add06550 Human Ckb  
Adfi14779 Human alb  
Aar76545 Human cir  
Adfi16471 Human alb  
Adfi16470 Human alb  
Add06587 Human Ckb  
Adfi16472 Human alb  
Adfi15550 Human alb  
Add06594 Human Ckb  
Adfi15095 Human alb  
Aaw17659 Stem cell  
Abu61830 Human che  
Add06589 Human Ckb  
Adfi14775 Human alb  
Adfi14773 Human alb  
Adfi15551 Human alb  
Adfi16474 Human alb  
Ade08053 HCC1 chem  
Adfi16539 Human alb  
Adfi15549 Human alb  
Add06595 Human Ckb  
Aao11593 Human pol  
Ade08943 Novel pro  
Adfi16552 Human alb  
Add06565 Human Ckb  
Add06591 Human Ckb  
Add06593 Human Ckb  
Adfi16476 Human alb  
Adfi16557 Human alb  
Adq66457 Novel hum  
Adfi14994 Human alb  
Adfi14995 Human alb  
Add06559 Human Ckb

99 385 76.4 676 7 ADD06562 Human Ckb  
100 385 76.4 691 7 ADF14999 Human alb

## ALIGNMENTS

## RESULT 1

AAR76128  
ID AAR76128 standard; protein; 93 AA.

XX AC AAR76128;  
XX 25-MAR-2003 (revised)  
DT 02-DEC-1995 (first entry)

XX Macrophage inflammatory protein-1-gamma.  
DE Macrophage inflammatory protein-1-gamma.  
XX Macrophage inflammatory protein-1-gamma; therapeutic; diagnostic.

XX Homo sapiens.  
XX Key Location/Qualifiers  
FT Peptide 1..24  
FT /note= "signal peptide"

XX WO9517092-A1.  
XX 29-JUN-1995.

XX 28-JUN-1994; 94WO-US007256.  
XX 22-DEC-1993; 93US-00173209.  
PR 08-MAR-1994; 94US-00208339.

XX (HUMA-) HUMAN GENOME SCI INC.  
XX Li H, Rosen CA, Ruben S, Adams MD;  
XX WPI; 1995-240404/31.  
DR N-PSDB; AAQ94094.

XX cDNA encoding human macrophage inflammatory proteins -3, -4 and -1 gamma  
PT - used in immuno-regulation including inflammatory activity,  
PT haematopoiesis, treatment of psoriasis or solid tumours.

XX Claim 48; Fig 8; 60pp; English.  
XX Human macrophage inflammatory protein-1-gamma (MIP-1g) is used in  
CC therapeutic and diagnostic applications for detecting and treating  
CC infections, cancer, inflammation, myelopietic dysfunction and autoimmune  
CC diseases. Antagonists/inhibitors of MIP-1g are used to treat diseases  
CC involving overexpression of MIP-1g, including silicosis,  
CC arteriosclerosis, autoimmune and chronic inflammatory and infective  
CC diseases, aplastic anaemia, etc. (Updated on 25-MAR-2003 to correct PN  
XX field.)

XX SQ Sequence 93 AA;  
Query Match 100.0%; Score 504; DB 2; Length 93;  
Best Local Similarity 100.0%; Pred. No. 1e-52;  
Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKISVAAIPFLLITLALGKTSSSRGYPHPSECCFTYTYKIPRQIMDYETNSQCS 60  
DB 1 MKISVAAIPFLLITLALGKTSSSRGYPHPSECCFTYTYKIPRQIMDYETNSQCS 60

QY 61 KPGIVFITKRGHVSCTNPSPDKWQDYIKDMKEN 93  
DB 61 KPGIVFITKRGHVSCTNPSPDKWQDYIKDMKEN 93

## RESULT 2

AAR95691  
ID AAR95691 standard; protein; 93 AA.

XX AC AAR95691;  
XX 20-DEC-1996 (first entry)  
XX Pituitary expressed chemokine (PGEC).  
XX Chemokine; liver; pituitary gland; LVEC; PGEC; inflammation; detection;  
KW identification; MCP receptor; CC-CKR1 receptor.  
XX Homo sapiens.  
XX WO9616979-A1.  
PD 06-JUN-1996.  
XX 29-NOV-1995; 95WO-US015484.  
XX 29-NOV-1994; 94US-00347492.  
XX (INCY-) INCYTE PHARM INC.  
XX Wilde CG, Hawkins PR, Bandman O, Seilhamer JJ, Neote KS;  
PI WPI; 1996-277714/28.  
DR N-PSDB; AAT31762.

XX liver and pituitary gland expressed chemokine(s) - useful for diagnosis  
PT of inflammation.  
XX Claim 1; Fig 7; 48pp; English.  
XX The nucleotide sequences encoding liver or pituitary expressed chemokines  
CC (LVEC or PGEC - See AAT31760-62) or primers derived from them, may be  
CC used for the detection of LVEC/PGEC encoding sequences in a biological  
CC sample. The presence of abnormal levels of the nucleotide sequences  
CC encoding LVEC's correlates highly with inflammation of the liver. The  
CC PGEC is used to selectively affect the CC-CKR1 receptor over the MCP  
CC receptor

XX SQ Sequence 93 AA;  
Query Match 100.0%; Score 504; DB 2; Length 93;  
Best Local Similarity 100.0%; Pred. No. 1e-52;  
Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKISVAAIPFLLITLALGKTSSSRGYPHPSECCFTYTYKIPRQIMDYETNSQCS 60  
DB 1 MKISVAAIPFLLITLALGKTSSSRGYPHPSECCFTYTYKIPRQIMDYETNSQCS 60

QY 61 KPGIVFITKRGHVSCTNPSPDKWQDYIKDMKEN 93  
DB 61 KPGIVFITKRGHVSCTNPSPDKWQDYIKDMKEN 93

RESULT 3  
AAW07203  
ID AAW07203 standard; protein; 93 AA.

XX AC AAW07203;  
XX 02-JUL-1997 (first entry)  
XX Human MIP-4: a chemoattractant for leukocytes.  
XX Leukocyte; attractant; affinity; leukaemia; immunity; wound healing;  
KW diagnosis; drug screening; inflammation; haematopoiesis regulator;  
KW psoriasis; stroke; thrombocytosis; pulmonary embolism; asthma; arthritis;  
KW aplastic anaemia; endotoxic shock; MIP; macrophage inflammatory protein.

XX Homo sapiens.

```

XX FH Key Location/Qualifiers
XX FT Peptide 1..19
XX FT /label= sig_peptide
XX FT Protein 20..93
XX FT /label= mat_protein
XX XX
XX FN WO9634891-A1.
XX XX
XX PD 07-NOV-1996.
XX XX
XX PF 23-JUN-1995; .95WO-US009058.
XX XX
XX PR 05-MAY-1995; .95US-00446881.
XX XX
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX XX
XX PI Rosen CA, Ruben SM, Li H, Adams MD;
XX XX
XX DR WPI; 1996-506106/50.
XX DR N-PSDB; AAT44362.
XX XX
XX PT New nucleic acid encoding the new human chemokine beta-8 - with
XX FT chemoattractant activity for leucocytes, for treating leukaemia,
XX FT stimulating immunity and wound healing, also for diagnosis and drug
XX FT screening.
XX XX
XX PS Example 2; Page 58; 93pp; English.
XX XX
XX CC Human macrophage inflammatory protein-4 (MIP-4) is an attractant for
XX CC leucocytes and is involved in the regulation of immune responses and
XX CC inflammation, e.g. stimulating synthesis of other cytokines. DNA encoding
XX CC MIP-4, MIP-4, and agonists of MIP-4 are useful for protecting bone marrow
XX CC against chemotherapeutic agents, for eliminating leukaemia cells (by
XX CC inducing apoptosis), stimulating an immune response and regulating
XX CC haematopoiesis (inhibiting proliferation and differentiation of cells)
XX CC and lymphocyte trafficking. MIP-4 is also used to treat psoriasis and
XX CC solid tumours; to increase host defences against chronic and acute
XX CC infection and to stimulate wound healing. MIP-4 also increase vascular
XX CC permeability, and can be used to treat stroke, thrombocytosis, pulmonary
XX CC embolism and myeloproliferative disease, and for identification of
XX CC specific receptors. Antagonists of MIP-4 are used to inhibit the
XX CC production of IL-1 and TNF-alpha and to treat e.g. aplastic anaemia,
XX CC myelodysplastic syndrome, asthma, arthritis (and many other autoimmune
XX CC and inflammatory diseases), infections, endotoxic shock, atherosclerosis,
XX CC allergy etc. MIP-4 and DNA encoding it may also be used in drug
XX CC development
XX XX
XX SQ Sequence 93 AA;
XX XX
XX Query Match 100.0%; Score 504; DB 2; Length 93;
XX Best Local Similarity 100.0%; Pred. No. 1e-52;
XX Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 MKISVAIPFLLITIALGTGTTSSSRGYPHPSCCFTYTYKIPRORIMDYETNSQCS 60
XX Db 1 MKISVAIPFLLITIALGTGTTSSSRGYPHPSCCFTYTYKIPRORIMDYETNSQCS 60
XX
XX Qy 61 KPGIVFITKRGHSVCTNPSPDKWQDYIKDMKEN 93
XX Db 61 KPGIVFITKRGHSVCTNPSPDKWQDYIKDMKEN 93
XX
XX RESULT 5
XX AAW57697
XX ID AAW57697 standard; protein; 93 AA.
XX AC AAW57697;
XX XX
XX DT 13-OCT-1998 (first entry)
XX DE Human M-CIF protein.
XX XX
XX KW Monocyte colony inhibitory factor; M-CIF; therapy; proliferation;
XX KW differentiation; low proliferative potential-colony forming cell;
XX KW colony forming unit-granulocyte; monocyte; chemotherapy; radiation;

```

```

XX Tandem gene; chemokine CC-2; chemokine CC-3; chemokine HCC-1; human;
XX KW cell migration; immune system.
XX OS Homo sapiens.
XX PN WO9741230-A2.
XX XX
XX PD 06-NOV-1997.
XX XX
XX PF 30-APR-1997; .97WO-EP002217.
XX XX
XX PR 30-APR-1996; .96DE-01017312.
XX XX
XX PA (FORS/) FORSMANN W.
XX XX
XX PI Forssmann W, Pardigol A, Maegert H, Schulz-Knappe P;
XX XX
XX DR WPI; 1997-549733/50.
XX DR N-PSDB; AAT95743.
XX XX
XX PT New nucleic acid of tandem human gene for chemokines CC-2 and CC-3 - used
XX FT for treating disorders of cell migration, the immune system and growth
XX FT functions.
XX XX
XX PS Claim 1; Page 16; 19pp; German.
XX XX
XX CC Novel nucleic acids of a tandem gene contain AAT95743 or AAT95744 and
XX CC encode the human chemokines CC-2 and CC-3. Transcription of the tandem
XX CC gene generates a bicistronic mature RNA containing two non-overlapping
XX CC open reading frames (ORF). AAT95743 has a 1st ORF for AAW38170, i.e. CC-
XX CC 2, and a 2nd ORF for AAW38171, i.e. the known chemokine HCC-1. AAT95744,
XX CC formed by alternative splicing of the primary transcript, has the same
XX CC 1st ORF but the 2nd encodes AAW38172, a variant form of HCC-1 having a 16
XX CC amino acid insertion, i.e. CC-3. The tandem gene has two functional
XX CC promoter regions, suggesting independent expression of the ORF. cDNA for
XX CC the bicistron was produced from the total RNA of T84 cells by 5'-rapid
XX CC amplification of complementary ends (RACE). The gene corresponding to
XX CC this DNA was isolated on chromosome 17, and found to have seven exons,
XX CC four for CC-2 and three for HCC-1/CC-3, separated by about 12 kb. CC-2
XX CC and CC-3 can be used to treat disorders of cell migration, the immune
XX CC system and growth functions. Also antibodies against them, and fragments
XX CC that hybridise to the cDNA, can be used for diagnosis. (Updated on 25-MAR
XX CC -2003 to correct PR field.)
XX XX
XX SQ Sequence 93 AA;
XX XX
XX Query Match 100.0%; Score 504; DB 2; Length 93;
XX Best Local Similarity 100.0%; Pred. No. 1e-52;
XX Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 MKISVAIPFLLITIALGTGTTSSSRGYPHPSCCFTYTYKIPRORIMDYETNSQCS 60
XX Db 1 MKISVAIPFLLITIALGTGTTSSSRGYPHPSCCFTYTYKIPRORIMDYETNSQCS 60
XX
XX Qy 61 KPGIVFITKRGHSVCTNPSPDKWQDYIKDMKEN 93
XX Db 61 KPGIVFITKRGHSVCTNPSPDKWQDYIKDMKEN 93
XX
XX RESULT 5
XX AAW57697
XX ID AAW57697 standard; protein; 93 AA.
XX AC AAW57697;
XX XX
XX DT 13-OCT-1998 (first entry)
XX DE Human M-CIF protein.
XX XX
XX KW Monocyte colony inhibitory factor; M-CIF; therapy; proliferation;
XX KW differentiation; low proliferative potential-colony forming cell;
XX KW colony forming unit-granulocyte; monocyte; chemotherapy; radiation;

```

```
KW myeloproliferative disorder; suppressor; inhibitor.
XX Homo sapiens.
XX WO9814582-A1.
XX 09-APR-1998.
XX
XX 30-SEP-1997; 97WO-US017505.
XX
XX 30-SEP-1996; 96US-0027299P.
XX 30-SEP-1996; 96US-0027300P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Gentz RL, Patel V, Kreider BL, Zhang J, Antonaccio M, Mendrick D;
XX Jimenez P;
XX WPI; 1998-240087/21.
XX N-PSDB; AAV24501.
XX
XX Inhibiting proliferation or differentiation of myeloid progenitor cells -
XX using myeloid progenitor inhibitory factor-1 amino-terminal deletion
XX mutant.
XX
XX Claim 79; Page 178; 298pp; English.
XX
XX This sequence represents a monocyte colony inhibitory factor (M-CIF)
XX which is used in a method for inhibiting proliferation or differentiation
XX of myeloid progenitor cells, specifically low proliferative potential-
XX colony forming cells or colony forming unit-granulocyte and monocyte
XX cells, in an human individual undergoing therapy that kills dividing
XX cells, especially chemotherapy or radiation therapy, where the
XX polypeptide results in accelerated recovery of platelets or granulocytes
XX alleviating thrombocytopenia or neutropenia. The polypeptide can be
XX administered to treat a myeloproliferative disorder, especially essential
XX thrombocyctosis, polycythemia vera and agnogenic myeloid metaplasia. The
XX polypeptide can also be used for myeloprotection, to inhibit growth of
XX hematopoietic progenitor cells, to treat sepsis, to suppress TNF-alpha
XX production, to treat renal injury, arthritis or joint inflammation,
XX enterocolitis or lupus
XX
XX Query Match 100.0%; Score 504; DB 2; Length 93;
XX Best Local Similarity 100.0%; Pred. No. 1e-52; Indels 0; Gaps 0;
XX Matches 93; Conservative 0; Mismatches 0;
XX
XX 1 MKISVAAIPFLLITIALGKTSSSRGYPHPSECCFTYTYKIPRQIMDYETNSQCS 60
XX |||||||
XX 1 MKISVAAIPFLLITIALGKTSSSRGYPHPSECCFTYTYKIPRQIMDYETNSQCS 60
XX
XX 61 KPGIVFTTKRGHSVCTNPSPDKWQDYIKDMKEN 93
XX |||||||
XX 61 KPGIVFTTKRGHSVCTNPSPDKWQDYIKDMKEN 93
XX
XX RESULT 6
XX AAB27659
XX ID AAB27659 standard; protein; 93 AA.
XX
XX AAB27659;
XX
XX 26-JAN-2001 (first entry)
XX
XX Human protein PRO877.
XX
XX Cardiovascular; endothelial; angiogenic disorder; PRO179; PRO238; PRO364;
XX PRO844; PRO846; PRO1760; PRO205; PRO321; PRO333; PRO840; PRO877; PRO878;
XX PRO879; PRO882; PRO885; PRO887; gene therapy.
XX
XX Homo sapiens.
XX
XX
```

```

FH Key Location/Qualifiers
FT Peptide 1..22
XX /label= Signal peptide
PN WO200053757-A2.
XX
XX 14-SEP-2000.
XX
XX 24-FEB-2000; 2000WO-US005004.
XX
XX 08-MAR-1999; 99WO-US005028.
XX 12-MAR-1999; 99US-0123957P.
XX 02-JUN-1999; 99WO-US012252.
XX 20-JUL-1999; 99US-0144758P.
XX 26-JUL-1999; 99US-0145698P.
XX 01-SEP-1999; 99WO-US020111.
XX 15-SEP-1999; 99WO-US021090.
XX 30-NOV-1999; 99WO-US028313.
XX 02-DEC-1999; 99WO-US028409.
XX 05-JAN-2000; 2000WO-US000219.
XX 18-FEB-2000; 2000WO-US004341.
XX 22-FEB-2000; 2000WO-US004342.
XX 22-FEB-2000; 2000WO-US004414.
XX
XX (GETH ) GENENTECH INC.
XX
XX Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Gerritsen ME;
XX Goddard A, Gurney AL, Hillan KJ, Marsters SA, Paoni NF, Pitti RM;
XX Watanabe CK, Williams PM, Wood WI;
XX WPI; 2000-611444/58.
XX N-PSDB; AAA99911.
XX
XX Novel PRO polypeptides and agonists and antagonists of them, used to
XX diagnose and treat cardiovascular, endothelial and angiogenic disorders.
XX
XX Claim 71; Fig 22; 181pp; English.
XX
XX The present invention relates to methods for stimulating or inhibiting
XX angiogenesis and cardiovascularization. The methods involve the use of
XX pharmaceutical compositions based on the following proteins, PRO179,
XX PRO238, PRO364, PRO844, PRO846, PRO1760, PRO205, PRO321, PRO333, PRO840,
XX PRO877, PRO878, PRO882, PRO885 or PRO887. These proteins were
XX identified by isolating cDNA clones encoding secreted proteins. The
XX proteins of the invention may be used to diagnose and treat
XX cardiovascular, endothelial or angiogenic disorders. The present sequence
XX is one of the proteins of the invention
XX
XX Sequence 93 AA;
XX
XX Query Match 100.0%; Score 504; DB 3; Length 93;
XX Best Local Similarity 100.0%; Pred. No. 1e-52; Indels 0; Gaps 0;
XX Matches 93; Conservative 0; Mismatches 0;
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XX 1 MKISVAAIPFLLITIALGKTSSSRGYPHPSECCFTYTYKIPRQIMDYETNSQCS 60
XX |||||||
XX 1 MKISVAAIPFLLITIALGKTSSSRGYPHPSECCFTYTYKIPRQIMDYETNSQCS 60
XX
XX 61 KPGIVFTTKRGHSVCTNPSPDKWQDYIKDMKEN 93
XX |||||||
XX 61 KPGIVFTTKRGHSVCTNPSPDKWQDYIKDMKEN 93
XX
XX RESULT 7
XX AAB15806
XX ID AAB15806 standard; protein; 93 AA.
XX
XX AAB15806;
XX
XX 17-JAN-2001 (first entry)
XX
XX Human chemokine HCC-1 SEQ ID NO: 48.
XX
XX
```



XX Macrophage recruitment; chemokine derivative; MCP-1; osteoporosis;  
 KW monocyte chemoattractant protein-1; inflammation; atherosclerosis; HIV;  
 KW AIDS; stroke; psoriasis; autoimmune disease; hypertension; endotoxaemia;  
 KW basophil-mediated disease; myocardial infarction; acute ischaemia;  
 KW rheumatoid arthritis; contraception.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200042071-A2.  
 XX 20-JUL-2000.  
 XX  
 XX 12-JAN-2000; 2000WO-US000821.  
 XX  
 XX 12-JAN-1999; 99US-00229071.  
 PR 17-MAR-1999; 99US-00271192.  
 PR 01-DEC-1999; 99US-00452406.  
 XX  
 XX (NEOR-) NEORX CORP.  
 XX  
 XX Grainger DJ, . Tatalick LM;  
 PI  
 XX WPI: 2000-499101/44.  
 DR N-PSDB; AAA74875.  
 XX  
 XX New peptide 3, amide and heterocyclic compounds and saccharide conjugates  
 PT used for inhibiting chemokine induced activity and for treating e.g.  
 PT stroke, vascular diseases, autoimmune diseases and tumor growth.  
 XX  
 XX Disclosure; Page 360-361; 387pp; English.  
 XX  
 CC The present invention concerns the identification of a number of  
 CC chemokines which can be used to produce derivatives, agonists and  
 CC antagonists which are then useful in disease treatment. The chemokines  
 CC include sequences AAB15785-B15794, AAB15803-B15813 and AAB15831-B15848.  
 CC These chemokine derivatives can be used to treat diseases such as  
 CC autoimmune diseases, atherosclerosis, osteoporosis, HIV infection and  
 CC AIDS, psoriasis, inflammatory diseases, hypertension, basophil-mediated  
 CC diseases, endotoxaemia, myocardial infarction, acute ischaemia and  
 CC rheumatoid arthritis, and can be used to prevent strokes and as  
 CC contraceptives. The coding sequences for the chemokines can be used in  
 CC gene therapy for the same diseases, as well as in the production of  
 CC animal models  
 XX  
 SQ Sequence 93 AA;  
 Query Match 100.0%; Score 504; DB 3; Length 93;  
 Best Local Similarity 100.0%; Pred. No. 1e-52;  
 Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 MKISVAIPFLLITIALGKTSSSRGYPHPSCCFTYTYTKIPRQIMDYETNSQCS 60  
 Db 1 MKISVAIPFLLITIALGKTSSSRGYPHPSCCFTYTYTKIPRQIMDYETNSQCS 60  
 Qy 61 KPGIVFITKRGHSVCTNPSPDKWQDYIKDMKEN 93  
 Db 61 KPGIVFITKRGHSVCTNPSPDKWQDYIKDMKEN 93  
 RESULT 8  
 AAB68294  
 ID AAB68294 standard; peptide; 93 AA.  
 XX  
 AC AAB68294;  
 XX  
 XX 09-JUL-2001 (first entry)  
 DT  
 XX  
 XX Amino acid sequence of a fragment of the chemokine PHC-1.  
 DE  
 XX Chemokine; PHC-1; chemokine receptor; CCR-5 receptor; inflammation;  
 KW cancer; restenosis; atherosclerosis; allergy; psoriasis; sarcoidosis;  
 KW chronic contact dermatitis; inflammatory bowel disease; stroke;  
 KW multiple sclerosis; organ transplant rejection; infection; wound healing;  
 KW bone healing; pain; diabetes; obesity; anorexia; bulimia; osteoporosis;  
 KW Parkinson's disease; acute heart failure; hypotension; hypertension;  
 KW urinary retention; angina pectoris; myocardial infarction; ischemia;  
 KW ulcer; migraine; vomiting; psychotic disorder; neurological disorder;  
 KW anxiety; schizophrenia; depression; delirium; dementia; dyskinesia;  
 KW mental retardation; degenerative disease; neurodegenerative disease;  
 KW Alzheimer's disease; Huntington's disease;  
 KW Gilles de la Tourette's syndrome.  
 XX  
 XX Synthetic.  
 XX  
 XX WO200131016-A2.  
 XX  
 XX 03-MAY-2001.  
 XX  
 XX 25-OCT-2000; 2000WO-BE000128.  
 XX  
 XX 25-OCT-1999; 99DE-01051336.  
 PR 22-JUN-2000; 2000EP-00870140.  
 XX  
 XX (EURO-) EUROSREEN SA.  
 PA (KIRC/) KIRCHHOFF F.  
 PA (FORS/) FORSMANN W.  
 XX  
 XX Forsemann W, Detheux M, Parmentier M, Staendker L;  
 PI WPI: 2001-308647/32.  
 XX  
 XX New processed human chemokines or their derivatives useful for preventing  
 PT and treating viral infections, inflammation, cancer, atherosclerosis,  
 PT multiple sclerosis, stroke, sarcoidosis or organ transplant rejection.  
 XX  
 XX Disclosure; Page 2; 50pp; English.  
 XX  
 CC The present sequence represents a fragment of an untruncated human  
 CC chemokine PHC-1. Peptides derived from truncated PHC-1 are inhibitors of  
 CC chemokine receptors, especially the CCR-5 receptor. Processed PHC-1  
 CC chemokines are useful for prevention and treatment of a disease induced  
 CC by viral infections, a bacterial agent or a protozoa. They are also  
 CC useful for prevention and/or the treatment of a disease such as  
 CC inflammation, cancers, restenosis, atherosclerosis, allergies, psoriasis,  
 CC chronic contact dermatitis, inflammatory bowel disease, multiple  
 CC sclerosis, stroke, sarcoidosis, organ transplant rejection, or infection  
 CC induced by pathogenic agent. They are also useful for wound and bone  
 CC healing, for treating pain, diabetes, obesity, anorexia, bulimia,  
 CC Parkinson's disease, acute heart failure, hypotension, hypertension,  
 CC urinary retention, osteoporosis, angina pectoris, myocardial infarction,  
 CC ischemia, ulcers, migraine, vomiting, psychotic and neurological  
 CC disorders, including anxiety, schizophrenia, depression, delirium,  
 CC dementia and severe mental retardation, degenerative diseases,  
 CC neurodegenerative diseases such as Alzheimer's disease, and dyskinesias  
 CC such as Huntington's disease or Gilles de la Tourette's syndrome  
 XX  
 SQ Sequence 93 AA;  
 Query Match 100.0%; Score 504; DB 4; Length 93;  
 Best Local Similarity 100.0%; Pred. No. 1e-52;  
 Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 MKISVAIPFLLITIALGKTSSSRGYPHPSCCFTYTYTKIPRQIMDYETNSQCS 60  
 Db 1 MKISVAIPFLLITIALGKTSSSRGYPHPSCCFTYTYTKIPRQIMDYETNSQCS 60  
 Qy 61 KPGIVFITKRGHSVCTNPSPDKWQDYIKDMKEN 93  
 Db 61 KPGIVFITKRGHSVCTNPSPDKWQDYIKDMKEN 93  
 RESULT 9  
 AAB50992  
 ID AAB50992 standard; protein; 93 AA.  
 XX

```
AC AAB50992;
XX
XX 21-MAR-2001 (first entry)
XX
XX Human PRO877 protein.
XX
XX Human; PRO; cardiac; antiangiogenic; antiarteriosclerotic; hypotensive;
XX vasotrophic; antiarthritis; antiarthritic; antiinflammatory; cytostatic;
XX vulnary; antianginal; gene therapy; cardiovascular disease;
XX endothelial disorder; angiogenic disorder; cancer; periodontal disease;
XX wound healing.
XX
XX Homo sapiens.
XX
XX WO200073445-A2.
XX
XX 07-DEC-2000.
XX
XX 17-MAY-2000; 2000WO-US013705.
XX
XX 02-JUN-1999; 99WO-US012252.
XX 23-JUN-1999; 99US-0141037P.
XX 20-JUL-1999; 99US-0144758P.
XX 26-JUL-1999; 99US-0145698P.
XX 28-JUL-1999; 99US-0146222P.
XX 01-SEP-1999; 99WO-US020111.
XX 30-NOV-1999; 99WO-US028313.
XX 30-NOV-1999; 99WO-US028409.
XX 02-DEC-1999; 99WO-US028565.
XX 16-DEC-1999; 99WO-US030095.
XX 05-JAN-2000; 2000WO-US000219.
XX 06-JAN-2000; 2000WO-US000376.
XX 11-FEB-2000; 2000WO-US000365.
XX 18-FEB-2000; 2000WO-US004341.
XX 18-FEB-2000; 2000WO-US004342.
XX 24-FEB-2000; 2000WO-US005004.
XX 02-MAR-2000; 2000WO-US005841.
XX 10-MAR-2000; 2000WO-US006319.
XX 15-MAR-2000; 2000WO-US006884.
XX 21-MAR-2000; 2000WO-US007532.
XX 30-MAR-2000; 2000WO-US008439.
XX
XX (GETH ) GENENTECH INC.
XX
XX Ashkenazi AJ, Baker KP, Ferrata N, Gerber H, Gerritson ME;
XX Goddard A, Godowski PJ, Gurney AL, Kuo SS, Mark MR, Marsters SA;
XX Pironi NF, Pitti RM, Watanabe CK, Williams PM, Wood WI;
XX
XX WPI; 2001-025251/03.
XX N-PSDB; AAC90576.
XX
XX Seventeen nucleic acids encoding PRO polypeptides which are useful in
XX diagnosis and treatment of cardiovascular, endothelial or angiogenic
XX disorders in a mammal.
XX
XX Claim 71; Fig 28; 182pp; English.
XX
XX The present sequence is one of seventeen novel PRO polypeptides. The PRO
XX nucleic acids, polypeptides, agonists and antagonists are useful for
XX treating cardiovascular, endothelial or angiogenic disorders in a mammal.
XX Examples of these disorders include cardiac hypertrophy, trauma, cancer,
XX age-related macular degeneration, atherosclerosis, hypertension, arterial
XX stenosis, Reynaud's disease, rheumatoid arthritis, angina, myocardial
XX infarctions, thrombophlebitis and lymphangitis. The PRO polypeptides and
XX antagonists are also used to prevent tumour angiogenesis and for treating
XX periodontal diseases. They are also used to stimulate wound healing and
XX tissue regeneration. The PRO nucleic acids, polypeptides and anti-PRO
XX antibodies are useful for diagnosing a cardiovascular, endothelial or
XX angiogenic disorder
XX
XX Sequence 93 AA;
SQ
Query Match 100.0%; Score 504; DB 4; Length 93;

Best Local Similarity 100.0%; Pred. No. 1e-52; Indels 0; Gaps 0;
Matches 93; Conservative 0; Mismatches 0;

QY 1 MKISVAAIPEFLLITIALGTKESSRGYPHPSECCFTYTKIPQRIMDYVETNSQCS 60
DB 1 MKISVAAIPEFLLITIALGTKESSRGYPHPSECCFTYTKIPQRIMDYVETNSQCS 60
QY 61 KPGIVFITKRGHSHVCTNPSPDKWQDYIKDMKEN 93
DB 61 KPGIVFITKRGHSHVCTNPSPDKWQDYIKDMKEN 93

RESULT 10
ABB90773
ID ABB90773 standard; protein; 93 AA.
XX
XX ABB90773;
XX
XX 30-MAY-2002 (first entry)
XX
XX Human Tumour Endothelial Marker polypeptide SEQ ID NO 279.
XX
XX Human; mouse; rat; TEM; tumour endothelial marker; NEM; PEM; cytostatic;
XX normal endothelial marker; pan-endothelial marker; immunostimulant;
XX antiangiogenic; tumour; neoangiogenesis; vascularised tumour;
XX polycystic kidney disease; diabetes; retinopathy; rheumatoid arthritis;
XX psoriasis.
XX
XX Homo sapiens.
XX
XX WO200210217-A2.
XX
XX 07-FEB-2002.
XX
XX 01-AUG-2001; 2001WO-US024031.
XX
XX 02-AUG-2000; 2000US-0222599P.
XX 11-AUG-2000; 2000US-0224360P.
XX 11-APR-2001; 2001US-0282850P.
XX
XX (UYJO ) UNIV JOHNS HOPKINS.
XX
XX St Croix B, Kinzler KW, Vogelstein B;
XX
XX WPI; 2002-291856/33.
XX N-PSDB; ABL92128.
XX
XX An isolated molecule comprising an antibody variable region which
XX specifically binds to an extracellular domain of a tumor endothelial
XX marker (TEM) protein, useful for inhibiting tumor growth.
XX
XX Claim 59; Page 283; 331pp; English.
XX
XX The invention relates to an isolated molecule comprising an antibody
XX variable region which specifically binds to an extracellular domain of a
XX tumour endothelial marker (TEM) protein selected from ABB90732, ABB90740,
XX ABB90749, ABB90750 and ABB90769. The antibodies which bind to TEM
XX proteins have cytostatic, immunostimulant and antiangiogenic activity.
XX They are useful for inhibiting tumour growth, neoangiogenesis in subjects
XX bearing a vascularised tumour, polycystic kidney disease, diabetic
XX retinopathy, rheumatoid arthritis and psoriasis. Human, mouse and rat TEM
XX genes and the encoded proteins (ABL92075-ABL92141 and ABB90721-ABB90789)
XX are disclosed, as are marker oligonucleotide sequences; tumour
XX endothelial markers (TEM) ABL91996-ABL92041 and ABL92143-ABL92191; normal
XX endothelial markers (NEM) ABL92042-ABL92074; and pan-endothelial markers
XX (PEM) ABL91903-ABL91995
XX
XX Sequence 93 AA;
SQ
Query Match 100.0%; Score 504; DB 5; Length 93;
Best Local Similarity 100.0%; Pred. No. 1e-52; Indels 0; Gaps 0;
Matches 93; Conservative 0; Mismatches 0;
```

Qy 1 MKISVAAIPFLLITIALGTTKTESSRGYPHPSECCFTYTYTKIPRIMDYETNSQCS 60  
Db 1 MKISVAAIPFLLITIALGTTKTESSRGYPHPSECCFTYTYTKIPRIMDYETNSQCS 60  
Qy 61 KPGIVFITKRGHVSCTNPSPDKWQDYIKDMKEN 93  
Db 61 KPGIVFITKRGHVSCTNPSPDKWQDYIKDMKEN 93

## RESULT 11

ABB90774  
ID ABB90774 standard; protein; 93 AA.

XX AC ABB90774;

XX DT 30-MAY-2002 (first entry)

XX DE Human Tumour Endothelial Marker polypeptide SEQ ID NO 281.

XX KW Human; mouse; rat; TEM; tumour endothelial marker; NEM; PEM; cytostatic;  
KW normal endothelial marker; pan-endothelial marker; immunostimulant;  
KW antiangiogenic; tumour; neoangiogenesis; vascularised tumour;  
KW polycystic kidney disease; diabetes; retinopathy; rheumatoid arthritis;  
KW psoriasis.

XX OS Homo sapiens.

XX PN WO200210217-A2.

XX PD 07-FEB-2002.

XX PF 01-AUG-2001; 2001WO-US024031.

XX PR 02-AUG-2000; 2000US-0222599P.

XX PR 11-AUG-2000; 2000US-0224360P.

XX PR 11-APR-2001; 2001US-0282850P.

XX PA (UYJO ) UNIV JOHNS HOPKINS.

XX PI St Croix B, Kinzler KW, Vogelstein B;

XX DR WPI; 2002-291856/33.

XX DR N-PSDB; ABL92129.

XX PT An isolated molecule comprising an antibody variable region which  
specifically binds to an extracellular domain of a tumor endothelial  
marker (TEM) protein, useful for inhibiting tumor growth.

XX PS Disclosure; Page 284; 331pp; English.

XX CC The invention relates to an isolated molecule comprising an antibody  
variable region which specifically binds to an extracellular domain of a  
tumor endothelial marker (TEM) protein selected from ABB90732, ABB90740,  
ABB90749, ABB90750 and ABB90769. The antibodies which bind to TEM  
proteins have cytostatic, immunostimulant and antiangiogenic activity.  
They are useful for inhibiting tumour growth, neoangiogenesis in subjects  
bearing a vascularised tumour, polycystic kidney disease, diabetic  
retinopathy, rheumatoid arthritis and psoriasis. Human, mouse and rat TEM  
genes and the encoded proteins (ABL92075-ABL92141 and ABB90721-ABB90789)  
are disclosed, as are marker oligonucleotide sequences: tumour  
endothelial markers (TEM) ABL91996-ABL92041 and ABL92143-ABL92191; normal  
endothelial markers (NEM) ABL92042-ABL92074; and pan-endothelial markers  
(PEM) ABL91903-ABL91995

XX SQ Sequence 93 AA;

Query Match 100.0%; Score 504; DB 5; Length 93;

Best Local Similarity 100.0%; Pred. No. 1e-52;

Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKISVAAIPFLLITIALGTTKTESSRGYPHPSECCFTYTYTKIPRIMDYETNSQCS 60

Db 1 MKISVAAIPFLLITIALGTTKTESSRGYPHPSECCFTYTYTKIPRIMDYETNSQCS 60

Qy 61 KPGIVFITKRGHVSCTNPSPDKWQDYIKDMKEN 93  
Db 61 KPGIVFITKRGHVSCTNPSPDKWQDYIKDMKEN 93

## RESULT 12

ABB90772

ID ABB90772 standard; protein; 93 AA.

XX AC ABB90772;

XX DT 30-MAY-2002 (first entry)

XX DE Human Tumour Endothelial Marker polypeptide SEQ ID NO 277.

XX KW Human; mouse; rat; TEM; tumour endothelial marker; NEM; PEM; cytostatic;  
KW normal endothelial marker; pan-endothelial marker; immunostimulant;  
KW antiangiogenic; tumour; neoangiogenesis; vascularised tumour;  
KW polycystic kidney disease; diabetes; retinopathy; rheumatoid arthritis;  
KW psoriasis.

XX OS Homo sapiens.

XX PN WO200210217-A2.

XX PD 07-FEB-2002.

XX PF 01-AUG-2001; 2001WO-US024031.

XX PR 02-AUG-2000; 2000US-0222599P.

XX PR 11-AUG-2000; 2000US-0224360P.

XX PR 11-APR-2001; 2001US-0282850P.

XX PA (UYJO ) UNIV JOHNS HOPKINS.

XX PI St Croix B, Kinzler KW, Vogelstein B;

XX DR WPI; 2002-291856/33.

XX DR N-PSDB; ABL92127.

XX PT An isolated molecule comprising an antibody variable region which  
specifically binds to an extracellular domain of a tumor endothelial  
marker (TEM) protein, useful for inhibiting tumor growth.

XX PS Disclosure; Page 282; 331pp; English.

XX CC The invention relates to an isolated molecule comprising an antibody  
variable region which specifically binds to an extracellular domain of a  
tumor endothelial marker (TEM) protein selected from ABB90732, ABB90740,  
ABB90749, ABB90750 and ABB90769. The antibodies which bind to TEM  
proteins have cytostatic, immunostimulant and antiangiogenic activity.  
They are useful for inhibiting tumour growth, neoangiogenesis in subjects  
bearing a vascularised tumour, polycystic kidney disease, diabetic  
retinopathy, rheumatoid arthritis and psoriasis. Human, mouse and rat TEM  
genes and the encoded proteins (ABL92075-ABL92141 and ABB90721-ABB90789)  
are disclosed, as are marker oligonucleotide sequences: tumour  
endothelial markers (TEM) ABL91996-ABL92041 and ABL92143-ABL92191; normal  
endothelial markers (NEM) ABL92042-ABL92074; and pan-endothelial markers  
(PEM) ABL91903-ABL91995

XX SQ Sequence 93 AA;

Query Match 100.0%; Score 504; DB 5; Length 93;

Best Local Similarity 100.0%; Pred. No. 1e-52;

Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKISVAAIPFLLITIALGTTKTESSRGYPHPSECCFTYTYTKIPRIMDYETNSQCS 60

Db 1 MKISVAAIPFLLITIALGTTKTESSRGYPHPSECCFTYTYTKIPRIMDYETNSQCS 60

Qy 61 KPGIVFITKRGHVSCTNPSPDKWQDYIKDMKEN 93

Db 61 KPGIVFITKRGHSVCTNPSPDKWQDYIKDMKEN 93

RESULT 13

ABU61834

ID ABU61834 standard; protein; 93 AA.

XX AC ABU61834;

XX DT 15-AUG-2003 (first entry)

XX DE Chemokine HCC1.

XX KW Chemokine; HCC1; cell development; tissue culture development.

XX OS Primates.

XX PN US2003028005-A1.

XX PD 06-FEB-2003.

XX PF 11-AUG-1999; 99US-00372348.

XX PR 12-AUG-1998; 98US-0096328P.

XX PA (BAZA/) BAZAN J F.

XX PI Bazan JF;

XX DR WPI; 2003-466159/44.

XX PN New composition comprising HCC5, Dub11, Dub12, primate MD1 or MD2 or rodent MD2 polypeptide, useful for modulating physiology or development of a cell or tissue culture cells.

XX PT Disclosure; Page 6-7; 77pp; English.

XX CC The invention relates to a novel chemokine, de-ubiquitination or cell surface protein. The composition is useful for modulating physiology or development of a cell or tissue culture cells. The present sequence represents the amino acid sequence of chemokine HCC1

XX CC Sequence 93 AA;

Query Match 100.0%; Score 504; DB 6; Length 93;

Best Local Similarity 100.0%; Pred. No. 1e-52;

Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKISVAAPFFLLITIALGKTSSSRGYPHPSECCFTYTYKIPRQIMDYETNSQCS 60

Db 1 MKISVAAPFFLLITIALGKTSSSRGYPHPSECCFTYTYKIPRQIMDYETNSQCS 60

Qy 61 KPGIVFITKRGHSVCTNPSPDKWQDYIKDMKEN 93

Db 61 KPGIVFITKRGHSVCTNPSPDKWQDYIKDMKEN 93

RESULT 14

ABU61832

ID ABU61832 standard; protein; 93 AA.

XX AC ABU61832;

XX DT 15-AUG-2003 (first entry)

XX DE Human MIP-4.

XX KW Human; MIP-4; cell development; tissue culture development.

XX OS Homo sapiens.

XX PN US2003028005-A1.

XX

Query Match 100.0%; Score 504; DB 6; Length 93;

Best Local Similarity 100.0%; Pred. No. 1e-52;

Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKISVAAPFFLLITIALGKTSSSRGYPHPSECCFTYTYKIPRQIMDYETNSQCS 60

Db 1 MKISVAAPFFLLITIALGKTSSSRGYPHPSECCFTYTYKIPRQIMDYETNSQCS 60

Qy 61 KPGIVFITKRGHSVCTNPSPDKWQDYIKDMKEN 93

Db 61 KPGIVFITKRGHSVCTNPSPDKWQDYIKDMKEN 93

PD 06-FEB-2003.

XX 11-AUG-1999; 99US-00372348.

XX 12-AUG-1998; 98US-0096328P.

XX PA (BAZA/) BAZAN J F.

XX PI Bazan JF;

XX DR WPI; 2003-466159/44.

XX PN New composition comprising HCC5, Dub11, Dub12, primate MD1 or MD2 or rodent MD2 polypeptide, useful for modulating physiology or development of a cell or tissue culture cells.

XX PT Disclosure; Page 6-7; 77pp; English.

XX CC The invention relates to a novel chemokine, de-ubiquitination or cell surface protein. The composition is useful for modulating physiology or development of a cell or tissue culture cells. The present sequence represents the amino acid sequence of human MIP-4

XX CC Sequence 93 AA;

Query Match 100.0%; Score 504; DB 6; Length 93;

Best Local Similarity 100.0%; Pred. No. 1e-52;

Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKISVAAPFFLLITIALGKTSSSRGYPHPSECCFTYTYKIPRQIMDYETNSQCS 60

Db 1 MKISVAAPFFLLITIALGKTSSSRGYPHPSECCFTYTYKIPRQIMDYETNSQCS 60

Qy 61 KPGIVFITKRGHSVCTNPSPDKWQDYIKDMKEN 93

Db 61 KPGIVFITKRGHSVCTNPSPDKWQDYIKDMKEN 93

RESULT 15

ABU61833

ID ABU61833 standard; protein; 93 AA.

XX AC ABU61833;

XX DT 15-AUG-2003 (first entry)

XX DE Pituitary expressed chemokine.

XX KW Pituitary expressed chemokine; chemokine; cell development;

XX OS Primates.

XX PN US2003028005-A1.

XX PD 06-FEB-2003.

XX PF 11-AUG-1999; 99US-00372348.

XX PR 12-AUG-1998; 98US-0096328P.

XX PA (BAZA/) BAZAN J F.

XX PI Bazan JF;

XX DR WPI; 2003-466159/44.

XX PN New composition comprising HCC5, Dub11, Dub12, primate MD1 or MD2 or rodent MD2 polypeptide, useful for modulating physiology or development of a cell or tissue culture cells.

XX PT Disclosure; Page 6-7; 77pp; English.

XX PS

CC The invention relates to a novel chemokine, de-ubiquitination or cell  
 CC surface protein. The composition is useful for modulating physiology or  
 CC development of a cell or tissue culture cells. The present sequence  
 CC represents the amino acid sequence of the pituitary expressed chemokine  
 CC  
 SQ Sequence 93 AA;

Query Match 100.0%; Score 504; DB 6; Length 93;  
 Best Local Similarity 100.0%; Pred. No. 1e-52;  
 Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKISVAALPFLITLITGKTSSSRGPHPSGCCFTYTYKIPRORIMDYETNSQCS 60  
 Db 1 MKISVAALPFLITLITGKTSSSRGPHPSGCCFTYTYKIPRORIMDYETNSQCS 60  
 Qy 61 KPGIVFITKRGHSVCTNPSPDKWQDYIKDMKEN 93  
 Db 61 KPGIVFITKRGHSVCTNPSPDKWQDYIKDMKEN 93

RESULT 16  
 ABUS4479  
 ID ABUS4479 standard; protein; 93 AA.  
 XX  
 AC ABUS4479;  
 DT 12-MAR-2003 (first entry)  
 XX  
 DE Human normal endothelial marker NEM 4.  
 XX  
 KW Human; endothelial cell; EC; tumour endothelial cell; TEM; NEM;  
 KW Tumour endothelial marker; normal endothelial marker; PEM;  
 KW pan-endothelial marker; polycystic kidney disease; psoriasis;  
 KW diabetic retinopathy; rheumatoid arthritis; tumour angiogenesis;  
 KW neovascularization; immune response; cytostatic; antidiabetic;  
 KW ophthalmological; antirheumatic; antiarthritic; antipsoriatic.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200283874-A2.  
 XX  
 PD 24-OCT-2002.  
 XX  
 PF 10-APR-2002; 2002WO-US008253.  
 XX  
 PR 11-APR-2001; 2001US-0282850P.  
 PR 06-FEB-2002; 2002US-0354262P.  
 XX  
 PA (UJJO ) UNIV JOHNS HOPKINS.  
 XX  
 PI Carson-Walter E, St Croix B, Kinzler KW, Vogelstein B;  
 PI  
 DR WPI; 2003-093016/08.  
 DR N-PSDB; ABX72052.  
 XX  
 PT New purified human transmembrane protein, designated as tumor endothelial  
 PT marker (TEM) 3, useful for detecting, diagnosing or treating tumors,  
 PT polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis or  
 PT psoriasis.  
 XX  
 PS Disclosure; Page 315; 374pp; English.  
 XX  
 CC The present invention relates to a novel method for the isolation of  
 CC endothelial cells (ECs), and the identification of genes expressed in  
 CC normal and tumour ECs. Tumour endothelial marker (TEM), normal  
 CC endothelial marker (NEM), and pan-endothelial marker (PEM) genes are  
 CC identified in human ECs. The human EC marker proteins and the  
 CC polynucleotide sequences encoding them are useful for detecting,  
 CC diagnosing or treating tumours as well as polycystic kidney disease,  
 CC diabetic retinopathy, rheumatoid arthritis, and psoriasis. They are also  
 CC useful for inhibiting neovascularization or tumour angiogenesis, for  
 CC inducing an immune response to tumour endothelial cells in a patient, or  
 CC for identifying candidate drugs for treating tumours. The present  
 CC invention represents a human chemokine or NEM protein of the invention

CC sequence represents a human TEM or NEM protein of the invention  
 XX  
 SQ Sequence 93 AA;

Query Match 100.0%; Score 504; DB 6; Length 93;  
 Best Local Similarity 100.0%; Pred. No. 1e-52;  
 Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKISVAALPFLITLITGKTSSSRGPHPSGCCFTYTYKIPRORIMDYETNSQCS 60  
 Db 1 MKISVAALPFLITLITGKTSSSRGPHPSGCCFTYTYKIPRORIMDYETNSQCS 60  
 Qy 61 KPGIVFITKRGHSVCTNPSPDKWQDYIKDMKEN 93  
 Db 61 KPGIVFITKRGHSVCTNPSPDKWQDYIKDMKEN 93

RESULT 17  
 ABUS4481  
 ID ABUS4481 standard; protein; 93 AA.  
 XX  
 AC ABUS4481;  
 DT 12-MAR-2003 (first entry)  
 XX  
 DE Human normal endothelial marker NEM 17.  
 XX  
 KW Human; endothelial cell; EC; tumour endothelial cell; TEM; NEM;  
 KW Tumour endothelial marker; normal endothelial marker; PEM;  
 KW pan-endothelial marker; polycystic kidney disease; psoriasis;  
 KW diabetic retinopathy; rheumatoid arthritis; tumour angiogenesis;  
 KW neovascularization; immune response; cytostatic; antidiabetic;  
 KW ophthalmological; antirheumatic; antiarthritic; antipsoriatic.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200283874-A2.  
 XX  
 PD 24-OCT-2002.  
 XX  
 PF 10-APR-2002; 2002WO-US008253.  
 XX  
 PR 11-APR-2001; 2001US-0282850P.  
 PR 06-FEB-2002; 2002US-0354262P.  
 XX  
 PA (UJJO ) UNIV JOHNS HOPKINS.  
 XX  
 PI Carson-Walter E, St Croix B, Kinzler KW, Vogelstein B;  
 PI  
 DR WPI; 2003-093016/08.  
 DR N-PSDB; ABX72054.  
 XX  
 PT New purified human transmembrane protein, designated as tumor endothelial  
 PT marker (TEM) 3, useful for detecting, diagnosing or treating tumors,  
 PT polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis or  
 PT psoriasis.  
 XX  
 PS Disclosure; Page 317; 374pp; English.  
 XX  
 CC The present invention relates to a novel method for the isolation of  
 CC endothelial cells (ECs), and the identification of genes expressed in  
 CC normal and tumour ECs. Tumour endothelial marker (TEM), normal  
 CC endothelial marker (NEM), and pan-endothelial marker (PEM) genes are  
 CC identified in human ECs. The human EC marker proteins and the  
 CC polynucleotide sequences encoding them are useful for detecting,  
 CC diagnosing or treating tumours as well as polycystic kidney disease,  
 CC diabetic retinopathy, rheumatoid arthritis, and psoriasis. They are also  
 CC useful for inhibiting neovascularization or tumour angiogenesis, for  
 CC inducing an immune response to tumour endothelial cells in a patient, or  
 CC for identifying candidate drugs for treating tumours. The present  
 CC invention represents a human TEM or NEM protein of the invention

Sequence 93 AA;

Query Match 100.0%; Score 504; DB 6; Length 93;  
Best Local Similarity 100.0%; Pred. No. 1e-52;  
Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKISVAAIPFFLLITLITGKTESSSRGYPHPSECCFTYTYKIPRQIMDYETNSQCS 60  
DB 1 MKISVAAIPFFLLITLITGKTESSSRGYPHPSECCFTYTYKIPRQIMDYETNSQCS 60

QY 61 KPGIVFITKRGHSVCTNPSPDKWQDYIKDMKEN 93  
DB 61 KPGIVFITKRGHSVCTNPSPDKWQDYIKDMKEN 93

RESULT 18  
ABU54480  
ID ABU54480 standard; protein; 93 AA.  
XX  
AC ABU54480;  
XX  
DT 12-MAR-2003 (first entry)  
XX  
DE Human normal endothelial marker NEM 14.  
XX  
KW Human; endothelial cell; EC; tumour endothelial cell; TEM; NEM;  
KW Tumour endothelial marker; normal endothelial marker; PEM;  
KW pan-endothelial marker; polycystic kidney disease; psoriasis;  
KW diabetic retinopathy; rheumatoid arthritis; tumour angiogenesis;  
KW neovascularization; immune response; cytostatic; antidiabetic;  
KW ophthalmological; antirheumatic; antiarthritic; antipsoriatic.  
XX  
OS Homo sapiens.  
XX  
PN WO200283874-A2.  
XX  
PD 24-OCT-2002.  
XX  
PF 10-APR-2002; 2002WO-US008253.  
XX  
PR 11-APR-2001; 2001US-0282850P.  
PR 06-FEB-2002; 2002US-0354262P.  
XX  
PA (UYJO ) UNIV JOHNS HOPKINS.  
XX  
XX Carson-Walter E, St Croix B, Kinzler KW, Vogelstein B;  
XX WPI; 2003-093016/08.  
XX N-PSDB; ABX72053.  
XX  
PT New purified human transmembrane protein, designated as tumor endothelial  
PT marker (TEM) 3, useful for detecting, diagnosing or treating tumors,  
PT polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis or  
PT psoriasis.  
XX  
PS Disclosure; Page 316; 374pp; English.  
XX  
CC The present invention relates to a novel method for the isolation of  
CC endothelial cells (ECs), and the identification of genes expressed in  
CC normal and tumour ECs. Tumour endothelial marker (TEM), normal  
CC endothelial marker (NEM), and pan-endothelial marker (PEM) genes are  
CC identified in human ECs. The human EC marker proteins and the  
CC polynucleotide sequences encoding them are useful for detecting,  
CC diagnosing or treating tumours as well as polycystic kidney disease,  
CC diabetic retinopathy, rheumatoid arthritis, and psoriasis. They are also  
CC useful for inhibiting neovascularization or tumour angiogenesis, for  
CC inducing an immune response to tumour endothelial cells in a patient, or  
CC for identifying candidate drugs for treating tumours. The present  
CC sequence represents a human TEM or NEM protein of the invention  
XX  
SQ Sequence 93 AA;

Query Match 100.0%; Score 504; DB 6; Length 93;  
Best Local Similarity 100.0%; Pred. No. 1e-52;

QY 1 MKISVAAIPFFLLITLITGKTESSSRGYPHPSECCFTYTYKIPRQIMDYETNSQCS 60  
DB 1 MKISVAAIPFFLLITLITGKTESSSRGYPHPSECCFTYTYKIPRQIMDYETNSQCS 60

QY 61 KPGIVFITKRGHSVCTNPSPDKWQDYIKDMKEN 93  
DB 61 KPGIVFITKRGHSVCTNPSPDKWQDYIKDMKEN 93

RESULT 19  
ABP76018  
ID ABP76018 standard; protein; 93 AA.  
XX  
AC ABP76018;  
XX  
DT 21-FEB-2003 (first entry)  
XX  
DE Human GENSET protein SEQ ID 225.  
XX  
KW Cytostatic; antiinflammatory; nootropic; neuroprotective; cardiant;  
KW gastrointestinal; gene therapy; GENSET; heavy metal toxicity; cancer;  
KW inflammatory disease; immune disorder; neuromuscular; toxicity;  
KW central nervous system; cardiovascular; gastrointestinal.  
XX  
OS Homo sapiens.  
XX  
PN WO200283898-A1.  
XX  
PD 24-OCT-2002.  
XX  
PF 18-APR-2001; 2001WO-IB000914.  
XX  
PR 18-APR-2001; 2001WO-IB000914.  
XX  
PA (GEST ) GENSET.  
XX  
PI Bejanin S, Tanaka H, Dumas Milne Edwards J, Jobert S, Giordano J;  
XX WPI; 2003-075548/07.  
XX  
PT New GENSET polynucleotides and polypeptides, useful for treating heavy  
PT metal toxicity, cancer, inflammatory diseases, immune disorders, and the  
PT neuromuscular, CNS, cardiovascular or gastrointestinal effects of the  
PT toxicity.  
XX  
PS Claim 14; Page 426; 735pp; English.  
XX  
CC The present invention relates to novel GENSET polynucleotides (ABZ36404-  
CC ABZ36911) encoding polypeptides (ABP75963-ABP76368). The polynucleotides  
CC and polypeptides are useful in screening and diagnostic assays for  
CC abnormal GENSET expression and/or biological activity. They are also  
CC useful for screening of compounds for treating or preventing GENSET-  
CC related disorders, such as heavy metal toxicity, cancer, inflammatory  
CC diseases, immune disorders, and the neuromuscular, central nervous system  
CC (CNS), cardiovascular or gastrointestinal effects of the toxicity  
XX  
SQ Sequence 93 AA;

Query Match 100.0%; Score 504; DB 6; Length 93;  
Best Local Similarity 100.0%; Pred. No. 1e-52;  
Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKISVAAIPFFLLITLITGKTESSSRGYPHPSECCFTYTYKIPRQIMDYETNSQCS 60  
DB 1 MKISVAAIPFFLLITLITGKTESSSRGYPHPSECCFTYTYKIPRQIMDYETNSQCS 60

QY 61 KPGIVFITKRGHSVCTNPSPDKWQDYIKDMKEN 93  
DB 61 KPGIVFITKRGHSVCTNPSPDKWQDYIKDMKEN 93



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DR WPI; 2003-598517/56.
DR N-PSDB; ADF15778.
XX
PT New albumin fusion protein, useful for preparing a composition for
PT treating diabetes mellitus.
XX
PS Example 4; SEQ ID NO 511; 24pp; English.
XX
CC This invention relates to a novel albumin fusion protein having albumin
CC or biological activity. Human serum albumin is responsible for a
CC significant proportion of the osmotic pressure of serum and also
CC functions as a carrier of endogenous and exogenous ligands. The fusion of
CC albumin to a therapeutic protein may increase shelf-life and stability of
CC the therapeutic protein. The albumin fusion protein of the invention may
CC allow production of compositions with antidiabetic activity whilst the
CC nucleotide sequence which encodes it may be useful for gene therapy. The
CC albumin fusion protein is useful for preparing a composition for treating
CC diabetes mellitus. The present sequence is that of a therapeutic protein
CC which was fused with human albumin to create a novel albumin fusion
CC protein of the invention. Note: The sequence data for this patent did not
CC form part of the printed specification, but was obtained in electronic
CC format directly from WIPO at ftp.wipo.int/pub/publishedpct_sequences
XX
SQ Sequence 93 AA;
Query Match 100.0%; Score 504; DB 7; Length 93;
Best Local Similarity 100.0%; Pred. No. 1e-52;
Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MKISVAAIPFLLITLITGKTSSSRGYPHPSECCFTYTYKIPQRIMDYETNSQCS 60
DB 1 MKISVAAIPFLLITLITGKTSSSRGYPHPSECCFTYTYKIPQRIMDYETNSQCS 60
QY 61 KPGIVFITKRGHSGVCTNPSPDKWQDYIKDMKEN 93
DB 61 KPGIVFITKRGHSGVCTNPSPDKWQDYIKDMKEN 93
RESULT 22
ADF16716
ID ADF16716 standard; protein; 93 AA.
XX
AC ADF16716;
XX
DT 12-FEB-2004 (first entry)
XX
DE Human albumin fusion protein-related protein SeqID1818.
XX
KW albumin fusion protein; albumin activity; human serum albumin;
KW serum osmotic pressure; shelf-life; stability; antidiabetic;
KW gene therapy; diabetes mellitus; human; gene; ds.
XX
OS Homo sapiens.
XX
PN WO2003060071-A2.
XX
PD 24-JUL-2003.
XX
PF 23-DEC-2002; 2002WO-US040891.
XX
PR 21-DEC-2001; 2001US-0341811P.
PR 24-JAN-2002; 2002US-0350358P.
PR 28-JAN-2002; 2002US-0351360P.
PR 28-FEB-2002; 2002US-0359370P.
PR 28-FEB-2002; 2002US-0360000P.
PR 27-MAR-2002; 2002US-0367500P.
PR 08-APR-2002; 2002US-0370227P.
PR 10-MAY-2002; 2002US-0378950P.
PR 24-MAY-2002; 2002US-0382617P.
PR 28-MAY-2002; 2002US-0383123P.
PR 05-JUN-2002; 2002US-0385708P.
PR 10-JUL-2002; 2002US-0394625P.
PR 24-JUL-2002; 2002US-0398008P.
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PR 09-AUG-2002; 2002US-0402131P.
PR 13-AUG-2002; 2002US-0402708P.
PR 18-SEP-2002; 2002US-0411355P.
PR 18-SEP-2002; 2002US-0411426P.
PR 02-OCT-2002; 2002US-0414984P.
PR 11-OCT-2002; 2002US-0417611P.
PR 23-OCT-2002; 2002US-0420246P.
PR 05-NOV-2002; 2002US-0423623P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
PA (DEL2 ) DELTA BIOTECHNOLOGY LTD.
PA (PRIN-) PRINCIPIA PHARM CORP.
XX
PI Ballance DJ, Turner AJ, Rosen CA, Haseltine WA;
XX
XX WPI; 2003-598517/56.
DR N-PSDB; ADF16390.
XX
XX New albumin fusion protein, useful for preparing a composition for
XX treating diabetes mellitus.
PT
XX
PS Example 4; SEQ ID NO 1818; 24pp; English.
XX
CC This invention relates to a novel albumin fusion protein having albumin
CC or biological activity. Human serum albumin is responsible for a
CC significant proportion of the osmotic pressure of serum and also
CC functions as a carrier of endogenous and exogenous ligands. The fusion of
CC albumin to a therapeutic protein may increase shelf-life and stability of
CC the therapeutic protein. The albumin fusion protein of the invention may
CC allow production of compositions with antidiabetic activity whilst the
CC nucleotide sequence which encodes it may be useful for gene therapy. The
CC albumin fusion protein is useful for preparing a composition for treating
CC diabetes mellitus. The present sequence is that of a therapeutic protein
CC which was fused with human albumin to create a novel albumin fusion
CC protein of the invention. Note: The sequence data for this patent did not
CC form part of the printed specification, but was obtained in electronic
CC format directly from WIPO at ftp.wipo.int/pub/publishedpct_sequences
XX
SQ Sequence 93 AA;
Query Match 100.0%; Score 504; DB 7; Length 93;
Best Local Similarity 100.0%; Pred. No. 1e-52;
Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MKISVAAIPFLLITLITGKTSSSRGYPHPSECCFTYTYKIPQRIMDYETNSQCS 60
DB 1 MKISVAAIPFLLITLITGKTSSSRGYPHPSECCFTYTYKIPQRIMDYETNSQCS 60
QY 61 KPGIVFITKRGHSGVCTNPSPDKWQDYIKDMKEN 93
DB 61 KPGIVFITKRGHSGVCTNPSPDKWQDYIKDMKEN 93
RESULT 23
ADF16713
ID ADF16713 standard; protein; 93 AA.
XX
AC ADF16713;
XX
XX 12-FEB-2004 (first entry)
DT
XX
XX Human albumin fusion protein-related protein SeqID1815.
XX
KW albumin fusion protein; albumin activity; human serum albumin;
KW serum osmotic pressure; shelf-life; stability; antidiabetic;
KW gene therapy; diabetes mellitus; human; gene; ds.
XX
OS Homo sapiens.
XX
PN WO2003060071-A2.
XX
PD 24-JUL-2003.
XX
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PF 23-DEC-2002; 2002WO-US040891.
XX
XX 21-DEC-2001; 2001US-0341811P.
PR 24-JAN-2002; 2002US-0350358P.
PR 28-JAN-2002; 2002US-0351360P.
PR 26-FEB-2002; 2002US-0359370P.
PR 28-FEB-2002; 2002US-0360000P.
PR 27-MAR-2002; 2002US-0367500P.
PR 08-APR-2002; 2002US-0370227P.
PR 10-MAY-2002; 2002US-0378950P.
PR 24-JUL-2002; 2002US-0394625P.
PR 09-AUG-2002; 2002US-0398008P.
PR 13-AUG-2002; 2002US-0402131P.
PR 18-SEP-2002; 2002US-0402708P.
PR 18-SEP-2002; 2002US-0411355P.
PR 02-OCT-2002; 2002US-0411426P.
PR 11-OCT-2002; 2002US-0414984P.
PR 23-OCT-2002; 2002US-0417611P.
PR 05-NOV-2002; 2002US-0423623P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
PA (DELZ ) DELTA BIOTECHNOLOGY LTD.
PA (PRIN-) PRINCIPIA PHARM CORP.
XX
XX Ballance DJ, Turner AJ, Rosen CA, Haseltine WA;
XX WPI; 2003-598517/56.
XX N-PSDB; ADF16387.
XX
XX New albumin fusion protein, useful for preparing a composition for
XX treating diabetes mellitus.
XX
XX Example 4; SEQ ID NO 1815; 24pp; English.
XX
XX This invention relates to a novel albumin fusion protein having albumin
XX or biological activity. Human serum albumin is responsible for a
XX significant proportion of the osmotic pressure of serum and also
XX functions as a carrier of endogenous and exogenous ligands. The fusion of
XX albumin to a therapeutic protein may increase shelf-life and stability of
XX the therapeutic protein. The albumin fusion protein of the invention may
XX allow production of compositions with antidiabetic activity whilst the
XX nucleotide sequence which encodes it may be useful for gene therapy. The
XX albumin fusion protein is useful for preparing a composition for treating
XX diabetes mellitus. The present sequence is that of a therapeutic protein
XX which was fused with human albumin to create a novel albumin fusion
XX protein of the invention. Note: The sequence data for this patent did not
XX form part of the printed specification, but was obtained in electronic
XX format directly from WIPO at ftp.wipo.int/pub/publishedpct_sequences
XX
XX Sequence 93 AA;
XX
XX Query Match 100.0%; Score 504; DB 7; Length 93;
XX Best Local Similarity 100.0%; Pred. No. 1e-52;
XX Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
Qy 1 MKISVAIPFLLITIALGTTSSSRGPHSPSCCTTYTKIPRQIMDYETNSQCS 60
Db 1 MKISVAIPFLLITIALGTTSSSRGPHSPSCCTTYTKIPRQIMDYETNSQCS 60
Qy 61 KPGIVFVTKRGHSVCTNPSPDKWQDYIKDMKEN 93
Db 61 KPGIVFVTKRGHSVCTNPSPDKWQDYIKDMKEN 93
XX
RESULT 24
ADFL6715
ID ADFL6715 standard; protein; 93 AA.
XX
XX AC ADFL6715;
XX
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XX 12-FEB-2004 (first entry)
XX
XX Human albumin fusion protein-related protein SeqID1817.
XX
XX albumin fusion protein; albumin activity; human serum albumin;
XX serum osmotic pressure; shelf-life; stability; antidiabetic;
XX gene therapy; diabetes mellitus; human; gene; ds.
XX
XX Homo sapiens.
XX
XX WO2003060071-A2.
XX
XX 24-JUL-2003.
XX
XX 23-DEC-2002; 2002WO-US040891.
XX
XX 21-DEC-2001; 2001US-0341811P.
PR 24-JAN-2002; 2002US-0350358P.
PR 28-JAN-2002; 2002US-0351360P.
PR 26-FEB-2002; 2002US-0359370P.
PR 28-FEB-2002; 2002US-0360000P.
PR 27-MAR-2002; 2002US-0367500P.
PR 08-APR-2002; 2002US-0370227P.
PR 10-MAY-2002; 2002US-0378950P.
PR 24-MAY-2002; 2002US-0382617P.
PR 28-MAY-2002; 2002US-0383123P.
PR 05-JUN-2002; 2002US-0385708P.
PR 10-JUL-2002; 2002US-0394625P.
PR 24-JUL-2002; 2002US-0398008P.
PR 09-AUG-2002; 2002US-0402131P.
PR 13-AUG-2002; 2002US-0402708P.
PR 18-SEP-2002; 2002US-0411355P.
PR 18-SEP-2002; 2002US-0411426P.
PR 02-OCT-2002; 2002US-0414984P.
PR 11-OCT-2002; 2002US-0417611P.
PR 23-OCT-2002; 2002US-0420246P.
PR 05-NOV-2002; 2002US-0423623P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
PA (DELZ ) DELTA BIOTECHNOLOGY LTD.
PA (PRIN-) PRINCIPIA PHARM CORP.
XX
XX Ballance DJ, Turner AJ, Rosen CA, Haseltine WA;
XX WPI; 2003-598517/56.
XX N-PSDB; ADF16389.
XX
XX New albumin fusion protein, useful for preparing a composition for
XX treating diabetes mellitus.
XX
XX Example 4; SEQ ID NO 1817; 24pp; English.
XX
XX This invention relates to a novel albumin fusion protein having albumin
XX or biological activity. Human serum albumin is responsible for a
XX significant proportion of the osmotic pressure of serum and also
XX functions as a carrier of endogenous and exogenous ligands. The fusion of
XX albumin to a therapeutic protein may increase shelf-life and stability of
XX the therapeutic protein. The albumin fusion protein of the invention may
XX allow production of compositions with antidiabetic activity whilst the
XX nucleotide sequence which encodes it may be useful for gene therapy. The
XX albumin fusion protein is useful for preparing a composition for treating
XX diabetes mellitus. The present sequence is that of a therapeutic protein
XX which was fused with human albumin to create a novel albumin fusion
XX protein of the invention. Note: The sequence data for this patent did not
XX form part of the printed specification, but was obtained in electronic
XX format directly from WIPO at ftp.wipo.int/pub/publishedpct_sequences
XX
XX Sequence 93 AA;
XX
XX Query Match 100.0%; Score 504; DB 7; Length 93;
XX Best Local Similarity 100.0%; Pred. No. 1e-52;
XX Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 MKISVAAIPFLLITLITGKTSSSRGYPHPSECCFTYTYTKIPRQIMDYETNSQCS 60  
 |||||  
 Db 1 MKISVAAIPFLLITLITGKTSSSRGYPHPSECCFTYTYTKIPRQIMDYETNSQCS 60  
 |||||  
 QY 61 KPGIVFITRKGHSVCTNPNPSDKWQDYIKDMKEN 93  
 |||||  
 Db 61 KPGIVFITRKGHSVCTNPNPSDKWQDYIKDMKEN 93  
 |||||

## RESULT 25

ADFI5205  
 ID ADFI5205 standard; protein; 93 AA.

XX AC ADFI5205;

DT 12-FEB-2004 (first entry)

XX Human albumin fusion protein-related protein SeqID503.

XX albumin fusion protein; albumin activity; human serum albumin;  
 KW serum osmotic pressure; shelf-life; stability; antidiabetic;  
 KW gene therapy; diabetes mellitus; human; gene; ds.

XX Homo sapiens.

XX PN WO2003060071-A2.

XX PD 24-JUL-2003.

XX PF 23-DEC-2002; 2002WO-US040891.

XX PR 21-DEC-2001; 2001US-0341811P.

PR 24-JAN-2002; 2002US-0350358P.

PR 28-JAN-2002; 2002US-0351360P.

PR 26-FEB-2002; 2002US-0359370P.

PR 28-FEB-2002; 2002US-0360000P.

PR 27-MAR-2002; 2002US-0367500P.

PR 08-APR-2002; 2002US-0370237P.

PR 10-MAY-2002; 2002US-0378950P.

PR 24-MAY-2002; 2002US-0382617P.

PR 28-MAY-2002; 2002US-0383123P.

PR 05-JUN-2002; 2002US-0385708P.

PR 10-JUL-2002; 2002US-0394625P.

PR 24-JUL-2002; 2002US-0398008P.

PR 03-AUG-2002; 2002US-0402131P.

PR 13-AUG-2002; 2002US-0402708P.

PR 18-SEP-2002; 2002US-0411355P.

PR 18-SEP-2002; 2002US-0411426P.

PR 02-OCT-2002; 2002US-0414984P.

PR 11-OCT-2002; 2002US-0417611P.

PR 23-OCT-2002; 2002US-0420246P.

PR 05-NOV-2002; 2002US-0423623P.

XX (HUMA-) HUMAN GENOME SCI INC.

PA (DELZ ) DELTA BIOTECHNOLOGY LTD.

PA (PRIN-) PRINCIPIA PHARM CORP.

XX Ballance DJ, Turner AJ, Rosen CA, Haseltine WA;

XX WPI; 2003-598517/56.

DR N-PSDB; ADFI5770.

XX New albumin fusion protein, useful for preparing a composition for  
 PT treating diabetes mellitus.

PS Example 4; SEQ ID NO 503; 24pp; English.

XX This invention relates to a novel albumin fusion protein having albumin  
 CC or biological activity. Human serum albumin is responsible for a  
 CC significant proportion of the osmotic pressure of serum and also  
 CC functions as a carrier of endogenous and exogenous ligands. The fusion of  
 CC albumin to a therapeutic protein may increase shelf-life and stability of

CC the therapeutic protein. The albumin fusion protein of the invention may  
 CC allow production of compositions with antidiabetic activity whilst the  
 CC nucleotide sequence which encodes it may be useful for gene therapy. The  
 CC albumin fusion protein is useful for preparing a composition for treating  
 CC diabetes mellitus. The present sequence is that of a therapeutic protein  
 CC which was fused with human albumin to create a novel albumin fusion  
 CC protein of the invention. Note: The sequence data for this patent did not  
 CC form part of the printed specification, but was obtained in electronic  
 CC format directly from WIPO at ftp.wipo.int/pub/publishedpct\_sequences  
 XX Sequence 93 AA;

Query Match 100.0%; Score 504; DB 7; Length 93;  
 Best Local Similarity 100.0%; Pred. No. 1e-52;  
 Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKISVAAIPFLLITLITGKTSSSRGYPHPSECCFTYTYTKIPRQIMDYETNSQCS 60

Db 1 MKISVAAIPFLLITLITGKTSSSRGYPHPSECCFTYTYTKIPRQIMDYETNSQCS 60

QY 61 KPGIVFITRKGHSVCTNPNPSDKWQDYIKDMKEN 93

Db 61 KPGIVFITRKGHSVCTNPNPSDKWQDYIKDMKEN 93

## RESULT 26

ADFI5332

ID ADFI5332 standard; protein; 93 AA.

XX AC ADFI5332;

XX DT 12-FEB-2004 (first entry)

XX Human albumin fusion protein-related protein SeqID631.

albumin fusion protein; albumin activity; human serum albumin;  
 KW serum osmotic pressure; shelf-life; stability; antidiabetic;  
 KW gene therapy; diabetes mellitus; human; gene; ds.

XX Homo sapiens.

XX PN WO2003060071-A2.

XX PD 24-JUL-2003.

XX PF 23-DEC-2002; 2002WO-US040891.

XX PR 21-DEC-2001; 2001US-0341811P.

PR 24-JAN-2002; 2002US-0350358P.

PR 28-JAN-2002; 2002US-0351360P.

PR 26-FEB-2002; 2002US-0359370P.

PR 28-FEB-2002; 2002US-0360000P.

PR 27-MAR-2002; 2002US-0367500P.

PR 08-APR-2002; 2002US-0370227P.

PR 10-MAY-2002; 2002US-0378950P.

PR 24-MAY-2002; 2002US-0382617P.

PR 28-MAY-2002; 2002US-0383123P.

PR 05-JUN-2002; 2002US-0385708P.

PR 10-JUL-2002; 2002US-0394625P.

PR 24-JUL-2002; 2002US-0398008P.

PR 09-AUG-2002; 2002US-0402131P.

PR 13-AUG-2002; 2002US-0402708P.

PR 18-SEP-2002; 2002US-0411355P.

PR 18-SEP-2002; 2002US-0411426P.

PR 02-OCT-2002; 2002US-0414984P.

PR 11-OCT-2002; 2002US-0417611P.

PR 23-OCT-2002; 2002US-0420246P.

PR 05-NOV-2002; 2002US-0423623P.

XX (HUMA-) HUMAN GENOME SCI INC.

PA (DELZ ) DELTA BIOTECHNOLOGY LTD.

PA (PRIN-) PRINCIPIA PHARM CORP.

XX



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PD 24-JUL-2003.
XX
XX 23-DEC-2002; 2002WO-US040891.
XX
XX 21-DEC-2001; 2001US-0341811P.
PR 24-JAN-2002; 2002US-0350358P.
PR 28-JAN-2002; 2002US-0351360P.
PR 26-FEB-2002; 2002US-0359370P.
PR 28-FEB-2002; 2002US-0360000P.
PR 27-MAR-2002; 2002US-0367500P.
PR 08-APR-2002; 2002US-0370227P.
PR 10-MAY-2002; 2002US-0378950P.
PR 24-MAY-2002; 2002US-0382617P.
PR 05-JUN-2002; 2002US-0385708P.
PR 10-JUL-2002; 2002US-0394625P.
PR 09-AUG-2002; 2002US-0402708P.
PR 13-AUG-2002; 2002US-0411355P.
PR 18-SEP-2002; 2002US-041426P.
PR 02-OCT-2002; 2002US-0414984P.
PR 11-OCT-2002; 2002US-0417611P.
PR 23-OCT-2002; 2002US-0420246P.
PR 05-NOV-2002; 2002US-0423623P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
PA (DELZ ) DELTA BIOTECHNOLOGY LTD.
PA (PRIN-) PRINCIPIA PHARM CORP.
XX
XX Ballance DJ, Turner AJ, Rosen CA, Haseltine WA;
PI
XX WPI; 2003-598517/56.
XX N-PSDB; ADF16388.
XX
XX New albumin fusion protein, useful for preparing a composition for
PT treating diabetes mellitus.
PT
XX Example 4; SEQ ID NO 1816; 24pp; English.
XX
XX This invention relates to a novel albumin fusion protein having albumin
CC or biological activity. Human serum albumin is responsible for a
CC significant proportion of the osmotic pressure of serum and also
CC functions as a carrier of endogenous and exogenous ligands. The fusion of
CC albumin to a therapeutic protein may increase shelf-life and stability of
CC the therapeutic protein. The albumin fusion protein of the invention may
CC allow production of compositions with antidiabetic activity whilst the
CC nucleotide sequence which encodes it may be useful for gene therapy. The
CC albumin fusion protein is useful for preparing a composition for treating
CC diabetes mellitus. The present sequence is that of a therapeutic protein
CC which was fused with human albumin to create a novel albumin fusion
CC protein of the invention. Note: The sequence data for this patent did not
CC form part of the printed specification, but was obtained in electronic
CC format directly from WIPO at ftp.wipo.int/pub/publishedpct_sequences
XX
XX Sequence 93 AA;
SQ
Query Match 100.0%; Score 504; DB 7; Length 93;
Best Local Similarity 100.0%; Pred. No. 1e-52;
Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MKISVAIPFLLITIALGKTESSRGYPHSPCCFTYTKIPRQIMDYETNSQCS 60
DB 1 MKISVAIPFLLITIALGKTESSRGYPHSPCCFTYTKIPRQIMDYETNSQCS 60
QY 61 KPGIVFTIKRGHSVCTNPSPDKWQDYIKDMKEN 93
DB 61 KPGIVFTIKRGHSVCTNPSPDKWQDYIKDMKEN 93
RESULT 29
ADF16739
ID ADF16739 standard; protein; 93 AA.
```

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XX
XX ADF16739;
XX
XX 12-FEB-2004 (first entry)
XX
XX Human albumin fusion protein-related protein SeqID1841.
DE
XX
XX albumin fusion protein; albumin activity; human serum albumin;
KW serum osmotic pressure; shelf-life; stability; antidiabetic;
KW gene therapy; diabetes mellitus; human; gene; ds.
XX
XX Homo sapiens.
OS
XX WO2003060071-A2.
XX
XX 24-JUL-2003.
XX
XX 23-DEC-2002; 2002WO-US040891.
XX
XX 21-DEC-2001; 2001US-0341811P.
PR 24-JAN-2002; 2002US-0350358P.
PR 28-JAN-2002; 2002US-0351360P.
PR 26-FEB-2002; 2002US-0359370P.
PR 28-FEB-2002; 2002US-0360000P.
PR 27-MAR-2002; 2002US-0367500P.
PR 08-APR-2002; 2002US-0370227P.
PR 10-MAY-2002; 2002US-0378950P.
PR 24-MAY-2002; 2002US-0382617P.
PR 05-JUN-2002; 2002US-0385708P.
PR 10-JUL-2002; 2002US-0394625P.
PR 09-AUG-2002; 2002US-0402131P.
PR 13-AUG-2002; 2002US-0402708P.
PR 18-SEP-2002; 2002US-0411355P.
PR 18-SEP-2002; 2002US-041426P.
PR 02-OCT-2002; 2002US-0414984P.
PR 11-OCT-2002; 2002US-0417611P.
PR 23-OCT-2002; 2002US-0420246P.
PR 05-NOV-2002; 2002US-0423623P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
PA (DELZ ) DELTA BIOTECHNOLOGY LTD.
PA (PRIN-) PRINCIPIA PHARM CORP.
XX
XX Ballance DJ, Turner AJ, Rosen CA, Haseltine WA;
PI
XX WPI; 2003-598517/56.
XX N-PSDB; ADF16413.
XX
XX New albumin fusion protein, useful for preparing a composition for
PT treating diabetes mellitus.
PT
XX Example 4; SEQ ID NO 1841; 24pp; English.
XX
XX This invention relates to a novel albumin fusion protein having albumin
CC or biological activity. Human serum albumin is responsible for a
CC significant proportion of the osmotic pressure of serum and also
CC functions as a carrier of endogenous and exogenous ligands. The fusion of
CC albumin to a therapeutic protein may increase shelf-life and stability of
CC the therapeutic protein. The albumin fusion protein of the invention may
CC allow production of compositions with antidiabetic activity whilst the
CC nucleotide sequence which encodes it may be useful for gene therapy. The
CC albumin fusion protein is useful for preparing a composition for treating
CC diabetes mellitus. The present sequence is that of a therapeutic protein
CC which was fused with human albumin to create a novel albumin fusion
CC protein of the invention. Note: The sequence data for this patent did not
CC form part of the printed specification, but was obtained in electronic
CC format directly from WIPO at ftp.wipo.int/pub/publishedpct_sequences
XX
XX Sequence 93 AA;
SQ
Query Match 100.0%; Score 504; DB 7; Length 93;
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 ID ADF15204 standard; protein; 93 AA.  
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 AC ADF15204;  
 XX  
 DT 12-FEB-2004 (first entry)  
 XX  
 DE Human albumin fusion protein-related protein SeqID502.  
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 KW albumin fusion protein; albumin activity; human serum albumin;  
 KW serum osmotic pressure; shelf-life; stability; antidiabetic;  
 KW gene therapy; diabetes mellitus; human; gene; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003060071-A2.  
 XX  
 PD 24-JUL-2003.  
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 PF 23-DEC-2002; 2002WO-US040891.  
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 PR 21-DEC-2001; 2001US-0341811P.  
 PR 24-JAN-2002; 2002US-0350358P.  
 PR 28-JAN-2002; 2002US-0351360P.  
 PR 26-FEB-2002; 2002US-0359370P.  
 PR 28-FEB-2002; 2002US-0360000P.  
 PR 27-MAR-2002; 2002US-0367500P.  
 PR 08-APR-2002; 2002US-0370227P.  
 PR 10-MAY-2002; 2002US-0378950P.  
 PR 24-MAY-2002; 2002US-0382617P.  
 PR 28-MAY-2002; 2002US-0383123P.  
 PR 05-JUN-2002; 2002US-0385708P.  
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 PR 24-JUL-2002; 2002US-0398008P.  
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 PR 18-SEP-2002; 2002US-0411355P.  
 PR 18-SEP-2002; 2002US-0411426P.  
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 PR 23-OCT-2002; 2002US-0420246P.  
 PR 05-NOV-2002; 2002US-0423623P.  
 XX  
 (HUMA-) HUMAN GENOME SCI INC.  
 PA (DELZ) DELTA BIOTECHNOLOGY LTD.  
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 XX  
 PI Ballance DJ, Turner AJ, Rosen CA, Haseltine WA;  
 XX  
 DR WPI; 2003-598517/56.  
 DR N-PSDB; ADF15769.  
 XX  
 PT New albumin fusion protein, useful for preparing a composition for  
 PT treating diabetes mellitus.  
 XX  
 PS Example 4; SEQ ID NO 502; 24pp; English.  
 XX  
 CC This invention relates to a novel albumin fusion protein having albumin  
 CC or biological activity. Human serum albumin is responsible for a  
 CC significant proportion of the osmotic pressure of serum and also

functions as a carrier of endogenous and exogenous ligands. The fusion of  
 CC albumin to a therapeutic protein may increase shelf-life and stability of  
 CC the therapeutic protein. The albumin fusion protein of the invention may  
 CC allow production of compositions with antidiabetic activity whilst the  
 CC nucleotide sequence which encodes it may be useful for gene therapy. The  
 CC albumin fusion protein is useful for preparing a composition for treating  
 CC diabetes mellitus. The present sequence is that of a therapeutic protein  
 CC which was fused with human albumin to create a novel albumin fusion  
 CC protein of the invention. Note: The sequence data for this patent did not  
 CC form part of the printed specification, but was obtained in electronic  
 CC format directly from WIPO at ftp.wipo.int/pub/publishedpct\_sequences  
 XX  
 SQ Sequence 93 AA;  
 Query Match 100.0%; Score 504; DB 7; Length 93;  
 Best Local Similarity 100.0%; Pred. NO. 1e-52;  
 Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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 DB 1 MKISVAAIPFFLLITIALGKTESSSRGYPHPSECCFTYTYTKIPRQRMIDYETNSQCS 60  
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 DB 61 KPGIVFITKRGHSVCTNPNSDKWQDYIKDMKEN 93  
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 Job time : 166 secs

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